OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

January 13, 2003, 09:53:15; Search time 31.9487 Seconds (without alignments) 58.391 Million cell updates/sec

Run on:

Title:

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AAM85222

ABB0761327

AAB71827

AAB47509

AAE14458

AAG23862

AAY21893

AAY21893

AAY21893

AAG42969

ABG42961

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ABB91938
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AAU51580
          AAU65960
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                                                       AAW60265
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Glycerol dehydrata
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                                                                   Klebsiella pneumon
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scoring table:
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Maximum DB seq length: 2000000000
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Maxim
Listing Iii

A Geneseq_101002:*

A [sins2/gcgdata/g
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3: /sins2/gcgdata/d
4: /sins2/gcgdata/d
4: /sins2/gcgdata/f
5: /sins2/gcgdata/f
6: /sins2/gcgdata/f
7: /sins2/gcgdat/g
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5: /SIDS2/gcgdata/genesed/geneseqp-emb1/AA1985.DAT:
7: /SIDS2/gcgdata/genesed/geneseqp-emb1/AA1986.DAT:
7: /SIDS2/gcgdata/genesed/geneseqp-emb1/AA1987.DAT:
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result NO. 1 1 2 3 3 7 7 10 10
Score 70 48 39 39 39 39 39
Query Query Match Length DB Match 12 100.0 14 2 68.6 79 2 55.7 28 2 55.7 28 2 55.7 28 2 55.7 28 3 55.7 28 3 55.7 28 3 55.7 28 3 55.7 28 3 55.7 28 3
14 79 79 28 28 28 28 28 28 28 28 28 28 28 28 28
222222222222222222222222222222222222222
AAY22918 AABB0610 ABB31012 ABB36201 ABB31577 AAM56983 AAM69369 AAM17202 AAM17202 AAM29695 AAM04898
Description  PSWTa linker pepti Environmental stre Peptide #363 enco Peptide #3707 enco Protein #3576 enco Protein #3576 enco Protein #3576 enco Human brain expres Human bone marrow Peptide #3636 enco Peptide #3732 enco Peptide #3580 enco

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AAY22918
                                                                                                                                                                                                                                  AAY22918 standard; peptide; 14 AA.
                                                                                                                                                                                                                    AAY22918;
                                                                                                                                                            peptide linker; fusion protein; pathogen resistance; pathogen tolerance;
plant; transgene; proteinase inhibitor; Arabidopsis thaliana;
                                                                                                                                                                                     PSMTa linker peptide used to make proteinase inhibitor fusions.
                                                                                                                                                                                                    19-AUG-1999 (first entry)
                                                                                                                                                       parasitic nematode.
                                                                                                                                         Synthetic.
                                                                                                                          WO9928484-A1.
                                                                                           01-DEC-1998;
                                                                                                           10-JUN-1999.
                                                                             03-DEC-1997;
                                                             (NOVS ) NOVARTIS AG.
Claim 10; Page 23; 39pp; English.
                proteinase inhibitor fusion proteins
                               WPI; 1999-385387/32.
                                             Atkinson HJ, McPherson MJ,
                                                                                97GB-0025556
                                                                                               98WO-EP07792.
                                                      Urwin PE;
                                                                                                                                                                                                                                                                                 ALIGNMENTS
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Polynucleotide sequences AAF74187 - AAF74218 encode proteins AAB80608 - AAB80639, which impart environmental stress resistance. The invention relates to a method for identifying DNA encoding proteins imparting environmental stress resistance. The method comprises inserting cell, culturing the transformants under conditions in which the untransformed host does not grow well, and selecting for viable clones are resistance factors. The DNA encoding proteins of the resistance factors. The DNA encoding proteins conferring environmental stress resistance, can be used in the production of plants resistant to environments such as deserts, salt damaged ground, cold regions and the oceans. They can be used for increasing the area of land covered by ground.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB80610
oceans. They can be used for increasing the area of land covered by green
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                                                                                                                                                                                                                                                                                        Claim 19; Page 83-84; 167pp; Japanese.
                                                                                                                                                                                                                                                                                                                        Screening method to obtain DNA encoding environmental stress resistance
                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF74189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamada A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUL-1999; 99JP-0235910.
24-MAR-2000; 2000JP-0085377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUL-2000; 2000WO-JP04862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200106006-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bruguiera sezangula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Environmental stress resistance; salt; heat; desert; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Environmental stress tolerant protein SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB80610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB80610 standard; Protein; 79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a peptide linker used in the fusion proteins of the invention. The specification describes a method for improving pathogen resistance or tolerance of a plant. The method are capable of improving pathogen in the plant with a transgene encoding a expressed on their own. Specifically, two or more protein or domains that inhibitors are co-delivered, as a fusion, to Arabidopsis thaliana. The proteins or domains are connected by a peptide linker. The method is descendants, especially against parasitic nematode attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-147355/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VILGVGPAKIQFEG 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ozeki Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Pred No. 1.1e-05;
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CC nucleic acid probes for measuring gene expression in a sample exon CC the probes with a collection of detectably labelled nucleic acid from mann breast and BT 474 cells. The method involves contacting CC derived from mann of detectably labelled nucleic acids CC derived from mann of his probes, and then measuring the label correct probe of the microarray. The probes are useful for CC expression of regions of genomic DAN predicted to CC expression analysis is useful for assessing the taxicity of chemical CC diversity of probes for measuring of this invention presents a far greater CC rapid production of functional information from genomic sequence. The cc probes of the control information from genomic sequence. The probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB31012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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                                                                                                                                                                                               The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                            Claim 27; SEQ ID NO 13980; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                            WPI; 2001-496933/54.
                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200157271-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #3663 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB31012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB31012 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plants, and desert greening and afforestation, in order to counter the effects of the increase in atmospheric carbon dioxide concentration. Primers AAF74219 and AAF74220 are used in an example illustrating the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 LVLGVGPERAHFEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VILGYGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.6%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AA

 3; Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _DB_22; Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR
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ABB36201
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                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
Вþ
                       QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                      Matches
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB36201 standard; Peptide; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #3707 encoded by human foetal liver single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB36201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157277-A2
                                                                                                                            The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, liver. The present sequence expression in samples derived from human measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2000;
                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 28836; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                               analyzing gene expression in human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 VLAVGPAQLQAE 18
                                                    Local Similarity es 7; Conserv
  7 VLAVGPAQLQAE 18
                           2 ILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 AA;
                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0633366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                            28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              2000GB-0024263
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.3%;
                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                      55.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
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                                                                       Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                            Mismatches
                                                                         DB 22;
6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                         Length 28;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RESULT 5
ABB21577
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ID AAM5
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                                                                                                                                                       γQ
XX
                                                                              RESULT 6
                                                                                                                                                                                            Matches
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB21577 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein #3576 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB21577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               congenital heart disease.
                                                                                                                                                                                                                                                                                 measuring human gene expression in a sample derived from human heart (set ABA21535-ABA41305). The present sequence is a protein encoded by one sucl ABA21535-ABA41305). The present sequence is a protein encoded by one sucl ABA21535-ABA41305). The present sequence is a protein encoded by one sucl probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. human heart and vascular system e.g. cardiovascular disease. hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
31-SAUG-2000; 2000US-0632366.
21-SAUG-2000; 2000US-0234687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US00666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 15; SEQ ID No 23347; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                         Sequence
               AAM56983;
                                               AAM56983 standard; Protein; 28 AA.
                                                                                                                                                           2 ILGYGPAKIQFE 13
                                                                                                                               7 VLAVGPAQLQAE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                            28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W,
                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                  Score 39; DB Pred. No. 6.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                         Length 28;
                                                                                                                                                                                                           Indels
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05-NOV-2001 (first entry)

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RESULT 7
AAM69369
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09-AUG-2001
                        WO200157276-A2
                                                               microarray; cancer; leukaemia; lymphoma; myeloma.
                                                  Homo sapiens.
                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 29675
                                                                        Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                       06-NOV-2001
                                                                                                                                                                   ААМ69369;
                                                                                                                                                                                   AAM69369 standard; Protein; 28 AA.
                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 29088; 650pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483446/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                  7 VLAVGPAQLQAE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human brain expressed single exon probe encoded protein SEQ ID NO: 29088.
                                                                                                                                                                                                                                                                           2 ILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                       28 AA;
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00667.
                                                                                                                                                                                                                                                                                                                55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W,
                                                                                                                                                                                                                                                                                                               Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                    DB 22; Length 28;
                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                         0;
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В Ωy

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RESULT 8
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                                                                               04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0233667.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-023559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
WPI; 2001-488901/53
                         Penn SG,
                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                   30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                       WO200157278-A2
                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                           12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                   cervical cancer.
                                                                                                                                                                                                                                                                                           Peptide #3636 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                      AAM17202;
                                                                                                                                                                                                                                                                                                                                                                        AAM17202 standard; Protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 29675; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VLAVGPAQLQAE 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tocal
                                                                                                                                                                                                                                                                   human; microarray; gene expression; cervical epithelial cell;
                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK,
                                                                    2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                    Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.7%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
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Pred. No. 6.8;
                      Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SENP: see AAI1068-AAI28459). The present sequence is a peptide encoder (SENP: see AAI1068-AAI28459). The present sequence is a peptide encoder by one such probe. The SENPs are derived from human HeLa cells. The SENI by one such probe as single exon microarray, which can be used for can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical measuring human gene expression, the probes are therefore epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably useful in grading and/or staging of diseases of the cervix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID No 22028; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #3732 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM29695 standard; Protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM29695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001.
                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00663
             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                               04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                      WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
predicting, measuring and displaying gene expression in samples derived
                                                                                                           analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VLAVGPAQLQAE 18
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                                                                                                              genome-derived single exon nucleic acid probes useful for
zing dene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 AA;
                                                                                                         gene expression in human placenta
                                                                                                                                                                                     Hanzel DK,
                                                                             SEQ ID No 29964; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                             ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0633366.
; 2000US-0234687.
; 2000US-0236359.
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Pred. No.
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AAM04898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                          Query Match
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM04898 standard; Protein; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probe; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #3580 encoded by probe for measuring breast gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM04898;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                             The present invention relates to novel single exon nucleic acid probes (see AA100010-AA110067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in such probes t sample, where the probe hypridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, stading, monitoring and prognosing predicting, diagnosing, grading, stading those diseases with polygenic diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, actiology. The diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.

In the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO as the form the proper action.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2001; 2001WO-US00661.
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                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID No 13638; 322pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                  Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                                                                                                                        in a human breast
                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
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                                                         Sequence
Local Similarity hes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
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                                                            28 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0236359
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                    55.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
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Pred. No.
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                    Score 39;
Pred. No.
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       Mismatches
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                         6.8;
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            Indels
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     nucleic acid expressed in the human lung; measuring gene expression in a collection of detectably labeled nucleic acids derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising of the array; identifying exons in a eukaryotic genome, comprising of the eukaryote; and (b) detecting at least one exon from genomic sequences labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, in the above mentioned microarray; assigning exons to a single exon probe, in the above mentioned microarray; assigning exons to a single gene, above and (b) measuring the expression of each of the exons in several tissues and/or cell types method the probes is included.
tissues and/or cell types using hybridisation to a single exon
                                                                                                                                                                                                                                   probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                                                                                                          12614 nucleic acid sequences mentioned in the specification, or the complements or the 12387 open reading frames derived from the 12614
                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of
                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 28650; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; pulmonary histiocytes; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytesis; lymphangioleiomyomtosis; Karagener syndrome; primary ciliary dyskinesis; pulmonary hypertension; humanica disease; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00665.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human peptide encoded by genome-derived single exon probe SEQ ID 28650.
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7 VLAVGPAQLQAE 18
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2000US-207456P
2000US-0608408
2000US-0632366
2000US-234687P
2000US-236359P
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RESULT 12
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01-APR-1999;
06-APR-1999;
                                          28-APR-1999;
30-APR-1999;
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16-APR-1999;
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09-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 34031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                 hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG28710 standard; Protein; 285 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene probes/open analysis, and for identifying exons in a gene, particularly such as asthma, lung derived mRNA and for the study of lung diseases (COPD), interstitlal lung disease (ILD), familial idiopathic pulmonary Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary hammonidarnosis mulmonary hietionurses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG28710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic and hyaline membrane disease. The present sequence is a peptide/protein note: The sequence data for this patent did not form part format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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99US-0132485
                                       9908-0132048
                                                                             99US-0130449.
99US-0130510.
                                                                   99US-0130891
                                                                                                         99US-0129845.
99US-0130077.
                                                                                                                                                99US-0128234.
                                                                                                                                                               99us-0127462
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58.3%;
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Pred. No. 6.8;
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99US-0139457 99US-013948 99US-0139461 99US-0139463 99US-0139863 99US-0139817 99US-0139817 99US-0140354 99US-0140354 99US-0140823 99US-0141842 99US-0141842 99US-0141842 99US-0142803 99US-0142977 99US-0142903 99US-0142977 99US-014291 99US-0143842 99US-0143842 99US-0144085 99US-0144085 99US-0144331 99US-0144333 99US-0144334 99US-0144334 99US-0144334 99US-0144334 99US-0144334	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
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NUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; AUG-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; SEP-1999; AUG-1999; AUG-19	19999 19999
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908-0159 908-01590 908-01510 908-01510 908-01510 908-01510 908-01510 908-01510 908-01510 908-01510 908-01530 908-01530 908-01530 908-01530 908-01540 908-01550 908-01550 908-01550 908-01550 908-01550 908-01550 908-01570 908-01580 908-01590 908-01590 908-01590 908-01590 908-01590 908-01590 908-01590 908-01590 908-01590 908-01590	014 014 0114 0114 0114 0114 0114 0114 0
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 60770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-2000 (first entry)
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                     99US-0121825

99US-0123480

99US-0123488

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99US-012814

99US-0130077

99US-0130510

99US-0130510

99US-0131449

99US-0132048

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99US-0161404
99US-0161406
99US-0161359
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Pred. No.
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27-JUL-1999 27-JUL-1999 28-JUL-1999 28-JUL-1999 02-AUG-1999 02-AUG-1999 02-AUG-1999 04-AUG-1999 04-AUG-1999 05-AUG-1999 05-AUG-1999 06-AUG-1999 06-AUG-1999 09-AUG-1999 09-AUG-1999

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RESULT 14
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26-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                        The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide SEQ
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                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                        useful as herbicides.
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243 VVVGGGPTGVEFSG 256
                                                                                                                      Local
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                                             1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; SEQ ID NO 1149;
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                                                                                                 Similarity 6; Conserv
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99US-0161359.
99US-0161360.
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99US-0162142.
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Pred. No. 1.5e+02;
                                                                                                                            Score 39; DB 23;
Pred. No. 1.5e+02;
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22-SEP-1999; 23-SEP-1999;

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24-SEP-1999; 28-SEP-1999; 29-SEP-1999; 04-OCT-1999; 05-OCT-1999; 06-OCT-1999; 07-OCT-1999;

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14-OCT-1999, 14-OCT-1999,

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18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 25-AUG-1999; 26-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999;

11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999;

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16-AUG-1999 17-AUG-1999

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Search completed: January 13, Job time: 33.9487 secs
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ABB90889
                                                                                                                   Query Match 55.7%;
Best Local Similarity 42.9%;
Matches 6; Conservative
                                                                                                                                                                                                     The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tietjen K, Weidler M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200210210-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herbicidally active polypeptide SEQ ID NO 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB90889 standard; Protein; 510 AA.
                                                        |::| || ::| |
245 VVVGGGPTGVEFSG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                    1 VILGVGPAKIQFEG 14
                                                                                                                                                                               510 AA;
            2003, 09:55:40
                                                                                                                Score 39; DB 23;
Pred. No. 1.5e+02;
4; Mismatches 4
                                                                                                                                            Length 510;
                                                                                                                   Indels
                                                                                                                  0;
                                                                                                                Gaps
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
   January 13, 2003, 09:53:20 ; Search time 12.9231 Seconds (without alignments) 104.146 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match Length DB
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Listing first 45 summaries
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S09098
S37240
       T10087
S48038
F70569
T07076
T07114
F91002
E85847
AE0164
B5A658
A13248
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S37239
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                                                                                                                     C; Keywords: metal binding
                                                                                                                                    A:Experimental source: leaves C:Superfamily: metallothionein
                                                                                                                                                A;Cross-references: EMBL:x91077; NID:gll50654; PIDN:CAA62551.1; PID:gll50655
                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-77 <FOL>
                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                  C:Accession: T12187
                                                                                                                                                                                                                                                                                                      C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                    metallothionein, type 1 - fava bean C; Species: Vicia faba (fava bean)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1993 .
A;Description: Sequence analysis of two cDNA clones for metallothionein-like proteins fu
                                                                   Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross_references: EMBL:226493; NID:g403328; PIDN:CAA81265.1; PID:g403329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-75 <ELL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Ellison, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Date: 06-Jan-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               metallothionein-like protein - white clover C; Species: Trifolium repens (white clover)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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C; Superfami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 2-4; 26-28; 39-42; 44-45; 47-48; 54-55 < KIW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A: Experimental source: cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Experimental source: cv. Feltham First A: Accession: $60719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession:
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                                                    Local [
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39 VVLGFGPAKIHFDG 52
                   1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                 36 VILGVGPAKIQFE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary
                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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                                                           Conservative
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                                                                       71.48;
                                                                                      80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.4%; Score 64; DB 2; I
100.0%; Pred. No. 0.00018;
tive 0; Mismatches 0;
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ative 0;
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                                                      Mismatches
                                                                     Score 56; I
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Pred. No. 1.5e-05;
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                                                                            DB 2; Length 77;
                                                                .0052;
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                                                   2;
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C; Keywords: metal binding
                          C;Comment: This protein participates in detoxification and metabolism of heavy metals C;Superfamily: metallothionein
                                                                                                         A; Molecule type: mRNA
A; Residues: 1-79 <KAW>
                                                                               A: Experimental source: seedling, cv.
                                                                                                                                              A; Reference number: JQ2128
A; Accession: JQ2128
                                                                                                                                                      R;Kawashima, I.; Inokuchi, Y.; Chino, M.; Kimura, M.; Shimizu, N.
Plant Cell Physiol. 32, 913-916, 1991
A;Title: Isolation of a gene for a metallothionein-like protein from soybean.
                                                                                                                                                                                                                       C;Species: Glycine max (soybean)
G;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 23-Mar-1995
C;Accession: JQ2128
                                                                                                                                                                                                                                                                                          metallothionein - soybean
                                                                                                                                                                                                                                                                                                                                                                                                     망
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-77 <ELL>
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A;Accession: S37239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1993
A;Description: Sequence analysis of two cDNA clones for metallothionein-like proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Ellison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metallothionein-like protein - white clover C; Species: Trifolium repens (white clover)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X58540; NID:g19006; PIDN:CAA41432.1; PID:g19007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RyOkumura, N.; Nishizawa, N.K.; Umehara, Y.; Mori, S. Plant Mol. Biol. 17, 531-533, 1991
A.Title: An iron deficiency-specific cDNA from barley r. A; Reference number: S17299; MUID:91355948; PMID:1832055
A; Accession: S17299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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A; Residues: 1-74 <OKU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Hordeum vulgare (barley)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 22-Jun-1999
C:Accession: S17299; S15558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metallothionein - barley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 9; Conserv
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Σ
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Similarity 69.2%;
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Pred. No. 0
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Pred. No. 0.018;
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70.08;

Score 49;

DB 2;

Length 79;

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R;Ledger, S.E.; Gardner, R.C.
Plant Mol. Biol. 25, 877-886, 1994
A;Title: Cloning and characterization of five cDNAs for genes
A;Reference number: S48035; MUID:94355660; PMID:8075403
A;Accession: S48038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: MTI
C;Superfamily: metallothionein
C;Keywords: metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Vangala, S.; Bailey-Serres, J.
Plant Physiol. 109, 721, 1995
A;Title: Nucleotide sequence of a maize (Zea mays L.) cDNA (Accession No. U29383) coding A;Reference number: Z16941; MUID:96030260; PMID:7480354
A;Accession: T10087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C;Accession: T10087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metallothionein-like protein - kiwi fruit
C;Species: Actinidia chinensis var. deliciosa (kiwi fruit)
C;Date: 26-Dec-1994 #sequence_revision 27-Feb-1997 #text_change 20-Aug-1999
C;Accession: S48038
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A; Residues: 1-80 < VAN>
A; Cross-references: EMBL: L02306; NID: 9169712; PID: 9169713
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hypothetical protein Rv3489 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: F70569
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-78 < LED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status:
                                                                                                                                                       F70569
                                                                                                                                                                           RESULT 10
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40 LIVGVAPQKTYFEG 53
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Local Similarity 57.1%;
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57.1%;
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3; Mismatches
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Pred. No. 1.3;
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Pred. No. 1
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A; Residues: 1-54 <COL>
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T07114
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A; Residues: 1-82 <WHI>
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A; Residues: 1-82 <GIR>
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metallothionein type II B - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Apr-2000
C;Accession: T07076
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A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Authors: Sqares, R; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Whitelaw, C.A.; LeHuquet, J.A.; Thurman, D.A.; Tomsett, A.B. submitted to the EMBL Data Library, July 1996
A;Description: The isolation and characterization of type II m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: metallothionein
C;Keywords: metal binding
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A;Experimental source: strain Ailsa craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z15900
A; Accession: T07076
                                                                                                                                                                                                                                                                                                                                                             metallothionein-like protein - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Experimental source: cultivar Bonner Best; root C; Superfamily: metallothionein C; Keywords: metal binding
                                                                                                                                                                                                                     R;Giritch, A.; Ganal, M.; Stephan, U.W.; Baumlein, H. Plant Mol. Biol. 37, 701-714, 1998
A;Title: Structure, expression and chromosomal localization A;Reference number: Z15923; MUID:98349862; PMID:9687073
                                                                                   A;Cross-references: EMBL:Z68138; NID:g1103688; PIDN:CAA92243.1; PID:g1103689
                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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60.0%;
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Pred. No.
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Pred. No.
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57.1%;

Score

40;

DB

2;

Length 82

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probable exported protein YPO1347 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                         В
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C;Superfamily: repressor protein cI
                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-215 <STO>
A;Cross-references: GB:AE005174; NID:gl2516411; PIDN:AAG57241.1; GSPDB:GN00145; UWGP:Z33
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                  AE0164
                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayheriller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein z3358 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli (c;Decies: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 03-Jun-2002 C;Accession: E85847
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A;Residues: 1-212 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36413.1; PID:g13362459; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gend A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91002
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Matches 7; Conserv
                                                                                                                                                                    60 LGVSPAKIMF 69
                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                            3 LGVGPAKIQF 12
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                                                                                                                                                                                                                                                              8;
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                                                                                                                                                                                                                                                              Conservative
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80.0%;
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80.0%;
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                                                                                                                                                                                                                                                                            Score 40; DB 2; Length 215; Pred. No. 12;
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C;Accession: AE0164
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
  B
                                           δÃ
                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-456 < KUR>
                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AE0164
                                                                                                                                                                                                  A; Gene:
                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                      A;Cross-references: GB:AL590842; PIDN:CAC90176.1; PID:g15979395; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                             Query Match 57.1%;
Best Local Similarity 72.7%;
Matches 8; Conservative
8 LILGAGPAAIQ 18
                                              1 VILGVGPAKIQ 11
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                                                                                                                 Score 40;
Pred. No.
                                                                                             Mismatches
                                                                                                                 DB 2;
26;
                                                                                                                                         Length 456;
                                                                                          Indels
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                                                                                       Gaps
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Search completed: January 13, 2003, 09:57:06 Job time: 14.9231 secs

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OM protein - protein search, using sw model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   January 13, 2003, 09:53:15; Search time 14 Seconds (without alignments) 41.476 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Match
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  Length DB
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MT1_CICAR
MT1A_VICFA
MT1_HORVU
MTA_TRIRP
MT2_RICCO
MT2_RCTCH
MT2_RCTCH
MT2_RCTCH
MT2_RCTCH
MT2_LCTCH
MT2_LCTCH
A4M1_HOMSE
A4M1_HOMSE
                                                                                                                                                                                                                                                                                                MT1B_VICFA
                                                                                                     NUSG_AQUAE
MRS4_YEAST
MRS3_YEAST
                                                                                                                                 6PGD_PIG
SAT_SYNY3
YLS4_CAEEL
                                                                                                                                                                              MT2B_LYCES
VIB5_AGRT5
                                                  PME_MEDSA
LRG1_YEAST
ATS2_BOVIN
ATS2_HUMAN
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ADH1_APTAU
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                                                                                                                                                                    MT2_VICEA
               MCA2_DROME
TIN2_MOUSE
LA_HUMAN
6PGD_HUMAN
                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                              Q41670 vicia faba p20830 pisum sativ p43399 trifolium r Q39456 cicer ariet Q41669 vicia faba p26571 hordeum vul p4398 trifolium r p30564 ricinus com p43390 actinidia c Q4167 mus musculu 000189 homo sapien Q40158 lycopersico p17795 agrobacteri q94029 oryza sativ p14332 sus scrofa p4241 synechocyst p34389 caenorhabdi 067757 aquifex aeo p23500 saccharomyc p10566 saccharomyc p10560 saccharomyc p10560 saccharomyc p10560 saccharomyc p10561 saccharomyc p105931 b adants-2
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                     Q9vur3
Q9qxg9
P05455
P52209
                                                       P79331 b adamts-2
095450 h adamts-2
            homo sapien
trifolium r
                                               drosophila
                               homo sapien
                                        mus musculu
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RESU MT1_ ID AC AC DT DT	Que Bes Mat Qy	DR DR DR DR SQ	000000000000000000000000000000000000000	RP RR R	OC SP OC SP OC SP	AC Q416 DT 01-NC DT 01-NC DT 15-JI	18_		35 35 35 35 35 35 35 36 36 37 44 44 44 44 44 44 44 44 44 44 44 44 44
ULT 2  PEA STANDARD; PRT; 75 AA.  P1830; P28830; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1991 (Rel. 17, Last sequence update) O1-FEB-1991 (Rel. 41, Last annotation update)	TY MATCH t Local Similarity 100.0%; Pred. No. 1.2e- t Local Similari	5. 1. multig 5A6A025BAA 3 70; DB 1	yright. It is prod of Bioinformatics Institute. There etions as long as is not removed. U agreement (See htt isb-sib.ch).	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  TISSUB-Leaf; MEDLINE-97238465; pubMed-9132050; MEDLINE-97238465; pubMed-9132050; Foley R.C. Liang 2.M., Singh K.B.; Foley R.C. Liang 2.M., Singh K.B.; Foley R.C. Liang 2.M., Singh K.B.; Foley R.C. Liang 3.M., Singh K.B.;  "Analysis of type 1 metallothionein cDNAs in Vicia faba."; "Analysis of type 33:583-591(1997) Plant Mol. Biol. 30:583-591(1997) Plant Mol. Biol. Biol. 30:583-591(1997) Plant Mol. Biol. Biol. Biol. Biol. 30:591(1997) Plant Mol. Biol. Bio	d bean). iplantae; streptophyta; Embryop iagnoliophyta; eudicotyledons; C iagnoliophyta; eudicotyledons; C iles; Fabaceae; papilionoideae;	0416/0; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Metallothionein-like protein 1B.		ALIGNMENTS	36 51.4 803 1 Z151_HUMAN 36 50.0 78 1 MT2_MUSAC 35 50.0 344 1 COMC_METUA 35 50.0 366 1 PHD1_YEAST 35 50.0 366 1 PHD1_YEAST 35 50.0 443 1 DCUA_HELPY 36 50.0 458 1 STHA_PSEAB 37 50.0 458 1 STHA_PSEAB 38 50.0 621 1 DCTB_RHIME 39 50.0 621 1 DCTB_RHIME 30 50.0 643 1 NOSZ_ALCEU
	0; Indels 0; Gaps 0;	ene family. CRC64; ; Length 75;	duced through a collaboration so and the EMBL outstation are no restrictions on its its content is in no way its content is in no way grape by and for commercial tp://www.isb-sib.ch/announce/	Caba."; DE CYSTEINE REAMILY; FAMILY 15.	phyta; Tracheophyta; core eudicots; Rosidae; Vicieae; Vicia.				Q13105 homo sapien Q2319 musa acumin Q28820 methanococc Q36093 saccharomyc Q43043 petunia int Q921c0 helicobacte Q92xp4 rhizobium m p57112 pseudomonas P46810 mycobacteri p13633 rhizobium m Q59105 alcaligenes

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MTB_TRIRP
ID MTB_TI
AC P4339;
DT 01-NO
DT 01-NO
DT 15-JU;
DE Metal.
GN MT1B.
OS TT1f6.
OC Eukar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                        Trifolium repens (Creeping white clover).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Trifolium.
              Ellison N.W., White D.W.R.; "Isolation of two cDNA clones encoding metallothionein-like proteins
(In) Plant Gene Register PGR96-068
                                                                       STRAIN=CV.
                                                                                                                                                                                                         MTB_TRIRP STANDARD; PRT; 75 AA. P43399; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                   Metallothionein-like protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metal-binding; Met
SEOUENCE 75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01439; Metallothio_2; 1.
Probom; PD001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 223097; CAA80645.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A plant metallothionein produced in E. coli.", FEBS Lett. 295:171-175(1991).
                                                                                                                                                                                                                                                                                                                                                                                     1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92111733; PubMed=1765150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 262:29-32(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans I.M., Gatehouse L.N., Gatehouse J.A., Robinson N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=cv. Feltham First; TISSUE=Root; MEDLINE=90201367; PubMed=2318309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pisum sativum (Garden pea)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $09098; $09098.
$20347; $20347
$20347; Metallothion_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene from pea (Pisum sativum L.) with homology to metallothionein
                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                           Huia; TISSUE=Stolon node;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7608 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 70; I
100.0%; Pred. No. 1
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ProDom; PD001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate Cluster.
SEQUENCE 75 AA; 7610 MW; 9B06F0CB(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

TISSUE-Etiolated epicoty1;

Dopico B., Labrador E., Ullan R.V., Munoz F.J.;

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE

RESIDUES THAT BIND VARIOUS HEAVY METALS

-i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                              EMBL; X95708; CAA65008.1; -
                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein-like protein 1 (MT-1).
Cicer arietinum (Chickpea) (Garbanzo).
Cicer arietinum (Chickpea) (Garbanzo)
36 VVLGVGPTKIHFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                            1 VILGYGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3827;
                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q39458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MT1_CICAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z26493; CAA81265.1; .
InterPro; IPR000347; Metallothion_15.
Pfam; PF01439; Metallothio_2; 1.
ProDom; PD001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate Cluster; Multigene family.
SEQUENCE 75 AA; 7659 MW; 64ACAACC234F54FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.
-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
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                                                                                 Similarity
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                                                                                                                                                                                     IPR000347; Metallothion_15.
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                                                                Conservative
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                                                                          85.7%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.4°,
100.08; Fi
                                                                         Score 60;
Pred. No.
                                                                                                                   9B06F0CB0B63F2BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 64; DB 1;
Pred. No. 0.000
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papilionoideae; Cicereae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 AA.
                                                                       .00069
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                                                                                 Length 75;
                                                   2; Indels
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                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                              Gaps
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                                            0;
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AC RELEASE REPORT OF THE PROPERTY OF THE PROPE
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Q41669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VICEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Vicieae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallothionein-like protein 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long to statement is in commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97238465; PubMed=9132050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Foley R.C., Liang Z.M., Singh K.B.; "Analysis of type 1 metallothionein cDNAs in Vicia faba."; plant Mol. Biol. 33:583-591(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000347; Metallothion_15.

Pfam; PF01439; Metallothion_2; 1.

ProDom; PD001611; Metallothion_15; 1.

Metal-binding; Metal-thiolate Cluster; Multigene family.

Metal-binding; Metal-thiolate Cluster; Multigene family.

SEQUENCE 77 AA; 8022 MW; 40CED53389EB8727 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X91077; CAA62551.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MT1_HORVU
                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallothionein-like protein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P26571;
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                      Okumura N., Nishizawa N.-K., Umehara Y., Mori S.;
"An iron deficiency-specific cDNA from barley roots having two homologous cysteine-rich MT domains.";
plant Mol. Biol. 17:331-533(1991).
                                                                                                                                             STRAIN=cv. Ehimehadaka No.1; TISSUE=Root; MEDLINE=91355948; PubMed=1832055;
                                                                                                                                                                                                                                                                                                                    spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         send an email to license@isb-sib.ch).
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.
SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 VVLGFGPAKIHFDG 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foca T
-1- FUNCTION: POSSIBLY RELEVANT TO MUGINEIC ACID-FAMILY (MAS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VILGYGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; Pr01439; Metallothio_2; 1.
Propom; PD001611; Metallothion_15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X58540; CAA41432.1; -.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SEQUENCE 74 AA; 7469 MW; F86C8CC3F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P43398;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionnidaaa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallothionein-like protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ellison N.W., White D.W.R.; "Isolation of two cDNA clones encoding metallothionein-like proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3899;
                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MAY HAVE A FUNCTION AT THE REGULATORY REGION OF MAS SYNTHETIC GENES OR FE(III) MAS TRANSPORTER GENE BY CONJUGATING WITH FE(2+) LIKE FUR PROTEIN.
                                                                                    EMBL; 226492; CAA81264.1; -.
InterPro; IPR000347; Metallothion_15.
pfam; PF01439; Metallothion_15; 1.
proDom; pD001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate cluster; Multigene family.
SEQUENCE 77 AA; 7503 MW; 5F4C163BA644BBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Trifolium repens L."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Gene Register PGR96-068.
FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Huia; TISSUE=Stolon node;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.7%;
69.2%;
                   75.7%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 53;
pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F86C8CC3F65901C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                          Score 53; DB 1;
pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.012;
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                                                             Length 77;
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MT2\_RICCO

MT2\_RICCO P30564;

RESULT 8

В

Matches

9;

Conservative

Mismatches

2;

Indels

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MT2_ACTCH STANDARD; PRT; 78 AA. P43390; PRT: 78 AA. 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Metallothionein-like protein type 2 PKIWI504. Proteinidia chinensis (Kiwi) (Yangtao).
                                                                            SEQUENCE FROM N.A.
STRAIN-CV. Deliciosa Hayward; TISSUE-Fruit;
                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Actinidiaceae; Actinidia
                                                                 Ledger S.E., Gardner R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000347; Metallothion_15.
Pfam; PF01439; Metallothio_2; 1.
ProDom; PD001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate cluster.
SEQUENCE 80 AA; 7953 MW; AA7304255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no was modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40 LVLGVGAEKAHFEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: METALLOTHIONEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (In) Plant Gene Register PGR95-066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of a class II metallothionein cDNA from Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis (Castor bean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metallothionein-like protein type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 IVMGVGSAKAQFEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komor E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7953 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.48;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA7304254491A3B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; [
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAVE A HIGH CONTENT OF CYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
0.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                         Best Local Similarity
                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MT2_CICAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RT
                                                                 Metal-binding; Metal-thiolate cluster; Multigene family.
SEQUENCE 79 AA; 7947 MW; OD8E6C8DBF356071 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                     Pfam; PF01439; Metallothio_2; 1.
ProDom; PD001611; Metallothion_15; 1.
                                                                                                                                                                         EMBL; x95709; CAA65009.1; ...
InterPro; IPR000347; Metallothion_15.
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             Metallothionein-like protein 2 (MT-2). Cicer arietinum (Chickpea) (Garbanzo). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  039459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01439; Metallothio_2; 1.
Prolom; PD001611; Metallothion 15; 1
Metal-binding; Metal-thiolate cluster.
SEQUENCE 78 AA; 7828 MW; EZFF9BEOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of five cDNAs for genes differentially expressed during fruit development of kiwifruit (Actinidia deliciosa var. deliciosa).";

Plant Mol. Biol. 25:877-886(1994).

-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS.

-!- DEVELOPMENTAL STAGE: HIGHLY EXPRESSED IN YOUNG FRUIT WITH REDUCED EXPRESSION IN THE LATER STAGES OF FRUIT DEVELOPMENT.

-!- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L27813; AAA53074.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 LIVGVAPQKTYFEG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CICAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000347; Metallothion_15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
          58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.0%;
57.1%;
Score 41; DB
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E2FF9BE0FFDD501D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 78;
                Length 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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MT2\_ACTCH

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Matches Query Match

InterPro;

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RESULT 11
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A4M1_HUMAN
ID A4M1_HI
AC 000189
DT 16-OCT
DT 16-OCT
                                                             RESULT 12
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A4M1_MOUSE STANDARD;
09JKC7;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Adapter-related protein complex 4 mu 1 subunit (Mu subunit of AP-4)
Adapter-related protein complex 4 mu 1 subunit (Mu subunit of AP-4)
Adapter-related protein complex 4 mu 1 subunit (Mu subunit of AP-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AP-4 adapter complex mu subunit) (Mu-adaptin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 LVMGVASGKTQFEG 53
                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                           EMBL; AF242858; AAF63513.1; -.
                                                                                                                                                                                                                               PROSITE; PS00990; CLAT_ADAPTOR_M_1; FALSE_NEG. PROSITE; PS00991; CLAT_ADAPTOR_M_2; FALSE_NEG.
                                                                                                                                                                                                         SEQUENCE
_AMI_HUMAN STANDARD; PRT; 453 AA
0001199; 09UHK9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
                                                                                                   396 LGLGPASLSFE 406
                                                                                                                                                   Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: ADAPTER-LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER COMPOSED OF TWO LARGE CHAINS (EPSILON/AP4E1 AND BETA/AP4B1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: ASSOCIATED WITH THE TRANS-GOLGI NETWORK (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM CHAIN (MU/AP4M1) AND A SMALL CHAIN (SIGMA/AP4S1) (BY
                                                                                                                             3 LGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY
                                                                                                                                                                                                                       pits;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                           449 AA;
                                                                                                                                                         Conservative
                                                                                                                                                                                                                       Endocytosis
                                                                                                                                                                                                           49509 MW; 579AEAE1F82B5D04 CRC64;
                                                                                                                                                                        58.6%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                     Score 41;
                                                                                                                                                                        Pred. No.
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449 AA
                                               453 AA
                                                                                                                                                                                        DB 1; Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
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                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                          NCBI_TaxID=9606;
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rissuE=Brain
                                                                                                                                         PROSITE; PS00990; CLAT_ADAPTOR_M_1; FALSE_NEG. PROSITE; PS00991; CLAT_ADAPTOR_M_2; FALSE_NEG.
                                                             SEQUENCE
                                                                                        CONFLICT
                                                                                                     CONFLICT
                                                                                                                    CONFLICT
                                                                                                                               Coated
                                                                                                                                                                              InterPro; IPR001392; Clathrn_med.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR MUARP2
                                                                                                                                                                                                                                                                                                                                                                             FAMILY.
                                                                                                                                                                                               602296;
                                                                                                                                                                    PF00928; Adap_comp_sub; 1.
                                                                                                                               pits;
                             Similarity
                                                                   453 AA;
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밁

Endocytosis.

400 417

R -> G (IN REF. 2 R -> Q (IN REF. 2 L -> M (IN REF. 2 S -> C (IN REF. 2

138B13A8C91D3444 CRC64;

58.6%; 63.6%; 50005 MW;

Score 41; pred. No.

DB 1; 9.1;

Length 453;

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15-JUN-2002 (Rel. 41, Last annotation update)
Adapter-related protein complex 4 mu 1 subunit (Mu subunit of AP-4)
(AP-4 adapter complex mu subunit) (Mu-adaptin-related protein 2) (mu-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99365166; PubMed=10436028;
Hirst J., Bright N.A., Rous B., Robinson M.S.;
"Characterization of a fourth adaptor-related protein complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97165966; PubMed=9013859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEBS Lett. 402:57-61(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEX, AP-4.";

J. Biol. Chem. 276:13145-13152(2001).

J. Biol. Chem. 276:13145-13145-13152(2001).

J. Biol. Chem. 276:13145-13145-13152(2001).

J. Biol. Chem. 276:13145-13145-13152(2001).

J. Biol. Chem. 276:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aguilar R.C., Boehm M., Gorshkova I., Crouch R.J., Tomita K., Saito T., Ohno H., Bonifacino J.S.; "Signal-binding specificity of the mud subunit of the adaptor protein "Signal-binding specificity of the mud subunit of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol. Cell 10:2787-2802(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of two new mu-adaptin-related proteins, mu-ARP1 and
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics institute. There are no restrictions on its buropean Bioinformatics institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: INTERACTS SPECIFICALLY WITH TYROSINE-BASED SORTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE ADAPTOR COMPLEXES MEDIUM SUBUNITS
                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                           EMBL; AF155158; AAD43328.1; -. EMBL; AF020796; AAD25869.1; -.
                                                                                                                                                                                   EMBL; Y08387; CAA69667.1;
Genew; HGNC:574; AP4M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: ADAPTER LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER SUBUNIT: ADAPTER LIKE COMPLEX 4 (AP-4) IS AN HETEROTETRAMER COMPOSED OF TWO LARGE CHAINS (EPSILON/AP461 AND BETA/AP461), AND DETA/AP461), AND MEDIUM CHAIN (MU/AP4M1) AND A SMALL CHAIN (SIGMA/AP461), MEDIUM CHAIN (MU/AP4M1) AND ASSOCIATED MITH THE TRANS-GOLGI NETWORK.
SUBCELLULAR LOCATION: ASSOCIATED MITH THE TRANS-COLGI NETWORK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: UBIQUITOUS. HI
LOWLY EXPRESSED IN BRAIN AND LUNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIGHLY EXPRESSED IN TESTIS AND
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B

Matches

7;

Conservative

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VIB5_AGRT5 STANDARD; PRT; 220 AA. P17795; O1-AUG-1990 (Rel. 15, Created) O1-AUG-1990 (Rel. 15, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                             Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Plasmid pTiC58.
                                                                                      VirB5 protein precursor.
VIRB5 OR ATU6171 OR AGR_PTI_9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; P0001611; Metallothion_15; 1.
Metal-binding; Metal-thiolate cluster; Multigene family.
CONFLICT 17 G -> D (IN REF. 2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this entrement is only as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000347; Metallothion_15
Pfam; PF01439; Metallothio_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L77966; AAB04675.1; -. EMBL; Z68138; CAA92243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giritch A., Herbik A., Balzer H., Stephan U., Baumlein H.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                           41 LVLGVGPEKTSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=cv. Bonner Beste; TISSUE=Root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Ailsa Craig; Whitelaw C.A., Lehuquet J.A., Thurman D.A., Tomsett A.B. Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MT2B_LYCES STANDARD; PRT; 82 AA Q40158; Q43514; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                              1 VILGVGPAKIOF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metallothionein-like protein type 2 B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 LGLGPASLSFE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESIDUES THAT BIND VARIOUS HEAVY METALS.
SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 AA; 8253 MW;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%;
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No. :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomsett A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
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                                                                Query Match
Best Local :
                                                                                                                                                          SIGNAL
                                                                                                                     SEQUENCE
                                                                                                                                                        Crown gall tumor; Plasmid; Signal; Complete proteome.
                                                                                                                                                                                                                  EMBL;
                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Eartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Gurson J., Lomo C., Sear C., Strub G., "Genome sequence of the plant pathogen and biotechnology agent Science 294:2323-2328(2001).

"In FUNCTION: VIEW PROFEISS ARE SUGGESTED TO ACT AT THE BACTERIAL THE PROFEISS ARE SUGGESTED TO ACT AT THE BACTERIAL
                                                                                                                                                                                           PIR; S12345; B5AG58.
                                                                                                                                                                                                                                                                  EMBL; X53264; CAA37358.1; -.
                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=21608550; PubMed=11743193;

WOOD D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
2 ILGVGPAKIQF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogowsky P.M., Powell B.S., Shirasu K., Lin T.-S., Morel P., Zyprian E.M., Steck T.R., Rado C.I.;
"Molecular characterization of the vir regulon of Agrobacterium tumefaciens: complete nucleotide sequence and gene organization of the 28.63-kbp regulon cloned as a single unit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90301800; PubMed=2194232;
MEDLINE=90301800; PubMed=2194232;
MEDLINE=90301800; Powell B.S., Shirasu K., Lin T.-S., Morel P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reading frames.";
Mol. Gen. Genet. 221:256-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=90318324; PubMed=2370849; Kuldau G.A., de Vos G., Owen J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kuldau G.A., de Vos G., Owen J., McCaffrey G., Zambryski P.;
"The virB operon of Agrobacterium tumefaciens pTiC58 encodes 11 open
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFER TO PLANT CELLS.
                                                                                                                                                                                                      J03320; AAA91595.1; -. AE009435; AAL46407.1; -. AE007923; AAK90933.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE AND THERE PLAY AN IMPORTANT ROLE IN DIRECTING T-DNA
                                                                                                             220 AA;
                                     Conservative
                                                                                                         220 V:
; 23269 MW;
                                                   55.7%;
63.6%;
                                                 Score 39;
Pred. No.
                                                                                                 VIRB5 PROTEIN.
; 78FFF913E03EA207 CRC64;
                                                                                                                                                POTENTIAL
                              Mismatches
                                                           DB 1; Length 220;
                          2;
                        Indels
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Q41657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vicia faba (Broad bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots; Rosid Spermatophyta; Magnoliophyta; eudicotyledons; Vicieae; Vicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metallothionein-like protein type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE-95036014; PubMed-7948889;

FOLEY R.C., Singh K.B.;

FOLEY R.C., Singh K.B.;

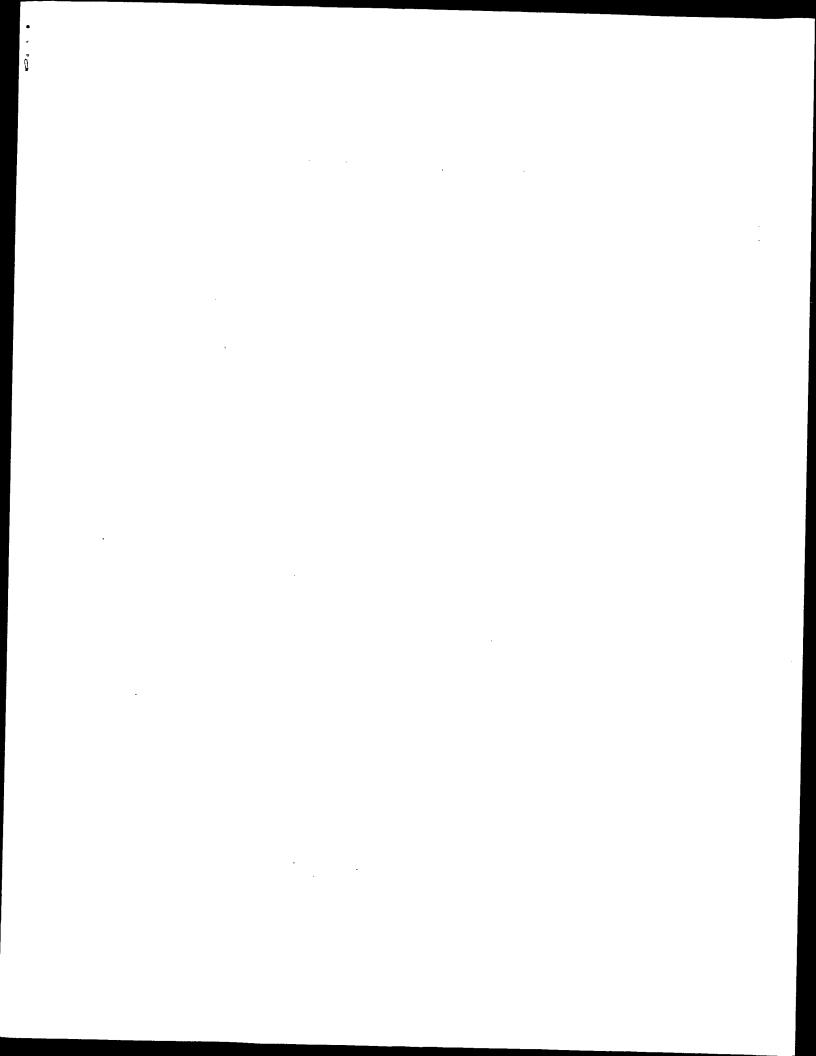
"Isolation of a Vicia faba metallothionein-like gene: expression in
                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3906;
                                                                                                                                                                                  InterPro; IPR000347; Metallothion_15.

Pfam; PF01439; Metallothion_2; 1.

ProDom; PD001611; Metallothion_15; 1.

Metal-binding; Metal-thiolate cluster; Multigene family.

SEQUENCE 77 AA; 7730 MW; 7D7BAD8D0223BF3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 15.
                                                                                                                                                                                                                                                                    EMBL; X77254; CAA54471.1;
                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| ||||: ||
15 LLSVGPARAQF 25
                                                                                                                        Local Similarity
nes 7; Conserva
                                                               40 LIMGYGSEKAQYE 52
                                                                                           1 VILGVGPAKIQFE 13
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                          54.3%; Score 38; DB 1; Length 77; 53.8%; Pred. No. 5.6;
                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 AA.
                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosidae;
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OM protein - protein search, using sw model

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:

Title: Perfect score:

US-09-554-941-11 73

1 QASIEGRYTAPQPQ 14 BLOSUM62 Gapop 10.0 , Gapext 0.5

scoring table: sequence:

Total number of hits satisfying chosen parameters:

908470 segs, 133250620 residues

post-processing: Minimum Match 08

Maximum Match 100% Listing first 45 summaries

Result No.

score

Match Length DB

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100.0

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73 45 43 43 42 42 42 42 42 41.5

58.9 57.5 57.5 57.5 57.5

283 105 313 474 493 69

ABB57844 ABB12235 ABB1223808 AAG23807 AAG23806 AAG23806 AAG23806

ABB39729

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pred. No. is the number of results predicted by chance to have a pred. No. is the number of result score of the result being printed, score greater than or equal to the score distribution.
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A. Geneseq_101002:*

A. G
                                                                                   Immunoglobulin lin
Hordeum vulgare ab
Hordeum vulgare ab
Human ORFX protein
Human ORFX prosophila melanog
Drosophila melanog
Human secreted pro
                                                                                                                                                                                            pescription
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Arabidopsis thalia
Arabidopsis thalia
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Human polypeptide
peptide #7235 enco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY22920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin linker used to make proteinase inhibitor fusions.
                                                                                                                                                                                                                                                                                                                                                                                                                      peptide linker; fusion protein; pathogen resistance; pathogen tolerance; peptide linker; proteinase inhibitor; Arabidopsis thaliana; plant; transgene; proteinase inhibitor; or note in the construction of th
                                                                                                                                                                                                                                                                                                                                                                                                         plant; transgene; p
parasitic nematode.
                                                                                                                                                                                                                                                                                                                                    WO9928484-A1.
                                                                                                                                                                                                                                                                                                                                                                         synthetic.
                                                                                                                                                                                                                                                                                                  10-JUN-1999.
                                                                                                                                                                                                                                                                01-DEC-1998;
                                                                                                                                                                                                                            03-DEC-1997; 97GB-0025556.
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                                                                                                                                                   Atkinson HJ, McPherson MJ, Urwin PE;
                                                                                                                     WPI; 1999-385387/32.
                                                                               proteinase inhibitor fusion proteins
                                            Claim 11; page 23; 39pp; English.
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Novel secreted pro
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Human secreted pro
Human colorectal c
Human polypeptide
Human polypeptide
Human protein sequ
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Novel human diagno
Novel human prote
Human foetal prote
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Human ORFX ORF1411
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Matches Query Match

4 IEGRYTAPOP 13 es 7; Conserv

Conservative

61.68; Score 45; DB 23; Length 321;

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The present invention describes an isolated barley aba45 promoter (I) comprising a 649 (ABA03924) or 587 (ABA03925) base pair sequence (I) a vector comprising (I) to 587 of ABA03925) base pair sequence (also comprising (I); (2) an isolated nucleic acid comprising the nucleic acids; and (4) a vector comprising the nucleic acids; and (4) a vector comprising a comprising the nucleic acids; and (4) a vector comprising a comprising the nucleic acids; and (4) a vector comprising the nucleic acids; and (4) a vector comprising the nucleic acids; and (4) a vector comprising the comprision of a vector comprision of a vector comprision of a vector comprision of a composition of a cost-effective means of decreasing hydrolytic enzymes in rice tissues of animal farming. Supplementation of hydrolytic enzymes in rice tissues in the composition of a cost-effective means of decreasing the environmental composition.
                                                                                                                                                                                                                                                                                                           New barley promoter sequence useful for expressing heterologous tissues to provide a cost-effective means of decreasing environmental impact of animal farming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABA03926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu J, Cheng K, Chen T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SINI-) ACAD SINICA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a peptide linker used in the fusion confirmed in the fusion. The specification describes a method for comprises transformation of the plant with a transgene encoding a for corporate of approving pathogen resistance or tolerance of a plant. The method for comprises to the plant with a transgene encoding a fullibitor are co-delivered, as a fusion, resistance or tolerance when that comparises two or more protein or domains that comprises are co-delivered, as a fusion, to harbidopsis that comparise or domains are connected by a peptide linker. The method is descendants, especially against parasition nomatons at the tolerance of a plant method is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hordeum vulgare cv. Himalaya; aba45; promoter; barley; plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare aba45 protein sequence SEQ ID NO:4.
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Pred. No. 2.1e-06;
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The present invention describes substantially purified human proteins of the red to as open reading frame, ORFX, where X is 1-11491 (see Table 1) reteins specification). ANNISTOS to ANNISTOS encode the human ORFX of sources in happologic to ANDISTOS encode the human ORFX proteins are useful for syndrome associated with ORFX proteins are useful for squences can be used in gene the therapy. ORFX proteins are useful for treatment of cancer, hyperproliferative disorder. ORFX polynucleotide of psoriasis, benign tumours, kaloid, degenerative disorders, cirrhosis of liver transplantation, cardiovascular diseases, diabetes mellitus, hemorrhage, the stranger of steps arythematosus, hypertension, hypothyroidss, disorders, haemorrhage, crange disease, various immune deficiencies and disorders, infectious
                                                                                                   Disclosure; SEQ ID 6182; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                  Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; degenerative disorder; psoriasis; benign tumour; cirrhosis; hypertension; hypertension; hypesase; diabetes mellitus; neurodegenerative disorder; immune deficiency; immune disorder; infectious disorder; autoimmune disorder; rheumatoid arthritis; autoimmune disorder; rheumatoid arthritis; autoimmune disorder; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ORFX protein sequence SEQ ID NO:6182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
                                                                         useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG1840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                    Disclosure; SEQ ID NO 324; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75
N-PSDB; ABL01947.
                                                                                                                                                                                                                                                                                                                                                              Venter JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 324.
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                                             The sequence data for this patent did not form specification, but was obtained in electronic
                                                                                                                                                                   capable of detecting 1000
                             at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                   TUCETACCTOUS -
                                                                                                                                                                                                                                                                                 New isolated nucleic acid
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                                                                                                                                                                                                                                                                from Drosophila and
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                              Li PWD,
                                                                                                                                                                     or more genes from Drosophila.
                                                                                                                                                                                                                                                                  detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cel
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Pred. No.
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                                                              part of the printed
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Best Local Similarity
The hes 7; Conserve
   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial isohaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; osteopathic; vasotropantifungal; vulnerary; antiulcer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                  e.g. arthritis and cancer
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
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chemotactic or chemokinetic
                     haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities;
                                                                                                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang YT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                    proteins and DNA encoding sequences useful for preventing, ing or ameliorating a medical condition in a mammalian subj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              secreted
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                                                                                                                                                                                                                                                                                                   Page 318; 1963pp; English.
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63.6%;
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       activities;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cc thrombolytic activities; receptor or ligand activities; or may be convolved in oncogenesis, cancer cell proliferation or metastasis.

Cc Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical cc conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell cd disorders), chronic inflammatory conditions (e.g., asthma or arthritis), cc proliferative retinopathy, atherosclerosis, coronary heart disease, cc arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal cc vascular growth. Polypeptides involved with tissue regeneration and crepair (or nucleic acids encoding them) may be used to promote wound concern the conditions and ulcers), while those with cc pacterial and fungal infections and ulcers), while those with cc pacterial and fungal infections in addition to immune disorders.

Cc promote cell growth. For example, such polypeptides may be used to promote cells of the used to augment or replace cells damaged by illness, cancerial acidsease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug corporated of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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   05-MAR-1999
09-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                          termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 27251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG23808 standard; Protein; 313 AA.
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82 QNGIPGEYTAPHP 94
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8; Conserva
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                99US-0129845.
99US-0130047.
99US-0130449.
99US-0130510.
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99US-0131449.
99US-0132048.
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99US-0127462.
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61.5%;
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Pred. No. 7.3;
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99US-0145085 99US-0145087 99US-0145192 99US-0145192 99US-0145218 99US-0145218 99US-0145276 99US-0145913 99US-0145913 99US-0145913 99US-0145919

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RESULT 7
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Similarity 53.8%;
7; Conservative
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390 QEGLAGRFTEPQP 402
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25-FEB-1999;
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99US-0134768.
99US-0134768.
99US-0134768.
99US-0134768.
99US-0134768.
99US-0134768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein; 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 42; DB;
pred. No. 40;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                               24-MAY-1999;
25-MAY-1999;
26-MAY-1999;
21-MAY-1999;
21-UN-1999;
21
                                                                         990S-0135629.
990S-0136921.
990S-013722.
990S-013722.
990S-0137528.
990S-0137528.
990S-0139540.
990S-0139454.
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990S-014963.
990S-0140853.
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990S-0144085.
990S-014433.
990S-014508.
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990S-014508.
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990S-014508.
990S-0145918.
990S-0145918.
990S-0145918.
990S-0145918.
990S-0145951.
990S-0145951.
990S-0145951.
990S-0145951.
990S-0145951.
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26-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
                                                                                                                                                                                                       10-SEP-1999;
                                                                                                                                                                                                                                                                                                                     10-AUG-1999,
                                                                                                                                                                                                                                                                                                                                                                  02-AUG-1999;
03-AUG-1999;
990S-0161359.
990S-0161360.
990S-0161361.
                990S-0160989
990S-0161404
990S-0161405
990S-0161406
                                    9908-0160981
                                                                       99US-0160741.
                                                                                      99US-0159331.
99US-0159637.
                                                                                                99US-0159330.
                                                                                                         99US-0159295.
                                                                                                                              99US-0158029.
99US-0158232.
                                                                                                                                             99us-0157753.
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99US-0151930
99US-0152363
99US-0153070
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990S-0148565
990S-0148684
990S-0149368
990S-0149175
990S-0149426
990S-0149426
990S-0149722
990S-0149723
990S-0149723
                                                                                                                                                                                                                                                                                                                      99US-0147416.
99US-0147493.
99US-0147935.
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99US-0147192.
99US-0147260.
99US-0147303.
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99US-0147038.
99US-0147204.
                                                                                                                                                                                                                                                                                                                  9908-0148171
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Query Match
                                                                                           The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, haematopoiesis regulating activity and may be useful in the diagnosis and/or inflammation cancer, leukaemia, nervous system disorders, arthrifis and
                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA013603
Local Similarity
hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЪ
                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 27495; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing algorithms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR
PR
                                                                                                                                                                                                                                                                                                                                            WPI; 2001-514838/56.
N-PSDB; AAI93534.
                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200164835-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 27495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA013603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAO13603 standard; Protein; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 QEGLAGRFTEPQP 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QASIEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 57.5%; Score 42; DB Local Similarity 53.8%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
    56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161992.
99US-0161993.
99US-0162142.
Score 41.5; DI
Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
        DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         o,
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Matches

Conservative

4; Mismatches

2

Indels Length 69;

Gaps

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1 QASIE-GRYTAPOPO 14

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RESULT 10
ABB39729
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                                                                                                                                                                 RESULT 11
XIX
                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB39729 standard; Peptide; 49 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide #7235 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        АВВЗ9729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a single exon nucleic acid probe for leasuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, neasuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly format from the contract of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 32364; 639pp + sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 QAGVQWGSYSSPQPQ 53
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                    06-NOV-2001
                                                                                                                  AAM73093 standard; Protein; 49
                                                                        AAM73093;
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                          20 VEGRHTVPRP 29
                                                                                                                                                                                                                                                                                         4 IEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312.
2000US-0207456.
                                                                                                                                                                                                                                                                                                                                           Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                       56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                  ω,.
                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 22; Length 49; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rank DR;
                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                         RESULT 12
                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 33399.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                   probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expression in bone marrow bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO: 33399; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                       Peptide #7349 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                 AAM33312 standard; Protein; 49
                                                                                                                                      genetic disorder
                                                                                                                                              Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                 17-OCT-2001 (first entry)
                                                                                                                                                                                                                           AAM33312;
04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
                                                                                      WO200157272-A2
                                   30-JAN-2001; 2001WO-US00663.
                                                              09-AUG-2001.
                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                              20 VEGRHTVPRP
                                                                                                                                                                                                                                                                                                                                      4 IEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                49 AA;
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0234687
2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                              56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                              Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 49
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                            30-JAN-2001; 2001WO-US00665
                                                                                                                                                                                                                                                          Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                 chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tubercus sclerosis; Gaucher's disease; Niemann-Pick disease; Lubercus sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                            15-NOV-2001.
                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                             Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease;
                                                                                                                                                                                                                                                                                                                                                                                     Human peptide encoded by genome-derived single exon probe SEQ ID 32604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG42939 standard; Peptide; 49 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG42939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 VEGRHTVPRP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 IEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULAR DYNAMICS INC.
                                             2000US-180312P
2000US-207456P
2000US-0608408
2000US-0632366
2000US-234687P
2000US-236359P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 33581; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                ABG07274
                                                                                                                                                                                                                                                                                                                                                                                                                                        CC mRNA, and (b) measuring the label detectably bound to each probe of CC (a) algorithmically predicting at least one exon from genomic sequences CC (a) algorithmically predicting at least one exon from genomic sequences CC of the eukaryote; and (b) detecting specific hybridisation of detectably CC having a fragment identical to the predicted exon, the probe is included CC comprising (a) identifying exons from genomic sequences CC having a fragment identical to the predicted exon, the probe is included CC comprising (a) identifying exons from genomic sequence by the method CC tissues and/or cell types using hybridisation to a single exon singular exons should be assigned to a single exon probe in the exons should be assigned to a single exon from genomic sequence by the method CC expression of the exons in the tissues and/or cell types indicates that CC in the exons should be assigned to a single gene; a peptide comprising one compression analysis, and for identifying exons in a gene, particularly such as asthma, lung derived mRNA and for the study of lung diseases (CCOPD), interstitial lung disease (ILD), familial idopathic pulmonary disease, hermansky-Pudlak syndrome, sarcoidosis, pulmonary alveolar proteinosis, tuberous sclerosis, Gaucher's disease, consultance of the intersticial primary ciliary dyskinesis, pulmonary hypertension encoded by a single exon probe of the invention.

CC of the printed specification, but was obtained in alactronic
                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Novel human diagnostic protein #7265.
                                             13-FEB-2002 (first entry)
                                                                                            ABG07274;
                                                                                                                            ABG07274 standard; Protein; 186 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one 12614 nucleic acid sequences mentioned in the specification, or their
                                                                                                                                                                                                                                          20 VEGRHTVPRP 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complements or the 12387 open reading frames derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 27; SEQ ID No 32604; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable set of single exon nucleic acid probes, used
                                                                                                                                                                                                                                                                                 4 IEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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60.0%;
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                                                                                                                                                                                                                                                                                                                                       Score 41; DB
Pred. No. 4.7;
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

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AAX22919
ID AAX222
XX AAX22
XX AAX22
XX 19-AU
XX 19-AU
XX Pepti
KW Pepti
KW Panat
KW Paras
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and CD polypeptide (II) sequences. (I) is useful as hybridisation probes, CD polymerase chain reaction (PCR) primers, oligomers, and for chromosome CD polynucleotides are also used in diagnostics as expressed sequence tags CD polynucleotides are also used in diagnostics as expressed sequence tags CD for identifying expressed genes. (I) is useful in gene therapy techniques CD for identifying expressed genes. (I) is useful in gene therapy techniques CD for identifying expressed genes. (I) as useful in gene therapy techniques CD for restore normal activity of (II) or to treat disease states involving CD for restore normal activity of (II) are useful in arkers and as CD food supplement. (II) and its binding partners are useful in medical CD imaging of sites expressing (II). (I) and (II) are useful for treating CD disorders involving aberrant protein expression or biological activity. CD The polypeptide and polynucleotide sequences have applications in CD classocies, forensics, gene mapping, identification of mutations cannot be produced to the treats of other traits to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/jpublished_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                Peptide linker; fusion protein; pathogen resistance; pathogen tolerance; plant; transgene; proteinase inhibitor; Arabidopsis thaliana;
                                                                                          Galactose oxidase linker used
                                                                                                                                                                                                       AAY22919 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                               19-AUG-1999
                                                                                                                                                                    AAY22919
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                 3 SIEGRYTAPQPQ 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; SEQ ID No 37633; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 AA;
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
                                                                                          to make proteinase inhibitor fusions.
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Search completed: January 13, 2003, 09:55:42 Job time: 32.9487 secs

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Best Local Similarity
                                                                                                                                     The present sequence represents a peptide linker used in the fusion proteins of the invention. The specification describes a method for improving pathogen resistance or tolerance of a plant. The method comprises transformation of the plant with a transgene encoding a fusion protein which comprises two or more protein or domains that are capable of improving pathogen resistance or tolerance when expressed on their own. Specifically, two distinct proteinase inhibitors are co-delivered, as a fusion, to Arabidopsis thaliana. The proteins or domains are connected by a peptide linker. The method is used to improve pathogen resistance or tolerance of a plant and its descendants, especially against parasitic nematode attack.
                                                                                                                                                                                                                                                                                                                  Claim 9;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-385387/32.
                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                             Proteinase inhibitor fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                      Atkinson HJ, McPherson MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                               (NOVS ) NOVARTIS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-DEC-1997;
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                         1 QASIEGRYTAPOPO 14
1 QAS---SYTAPQPQ 11
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                                                                                                              11 AA;
                                                       Conservative
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71.4%;
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OM protein - protein search, using sw model
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Maximum DB
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                                                                                                                                                                     Score
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seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_rvirus:*
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023812
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              Q9fr40 petunia hyb
Q8wv65 homo sapien
Q8wv65 mycobacteri
Q80335 citrus unsh
Q94i98 atropa bell
Q92r37 rhizobium m
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     Q9eyb2
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## ALIGNMENTS

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RESULT 1
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ID QSSP3
ID QSSP3
AC QSSP
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DT 01-M
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T Type
GN METIT
OC Euke
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RESULT 2
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Potenza C., Thomas S.H., Sengupta-Gopalan C.;
Potenza C., Thomas S.H., Sengupta-Gopalan C.;
Potenza Induced during early response to Meloidogyne incognita in roots
of resistant and susceptible alfalfa cultivars.";
Plant Sci. 161:289-299(2001).
EMBL; ASI89766; AAR704584.1;
InterPro; IPR000347; Metallothion_15.
ProDom; PD01439; Metallothion_15; 1.
ProDom; PD01611; Metallothion_15; 1.
SEQUENCE 75 AA; 7537 MW; 7872EFOFOZBD22FB CRC64;
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Q9SP23; Q1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago sativa (Alfalfa).

Medicago sativa (Alfalfa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; core eudicots; Rosidae

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae

Spermatophyta; Magnoliophyta; Papilionoideae; Trifolieae; Medicago.
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RESULT 3
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                                                                                                                                                                                                                                                                                                                  InterPro; IPR000347; Metallothion_15. Pfam; PF01439; Metallothio_2; 1. ProDom; PD001611; Metallothion_15; 1. SEQUENCE 75 AA; 7831 MW; A772B9B99367755A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Itai A., Tanaka T., Tanabe K., Tamura F., "Pyrus pyrifolia ripening associated mRNA, clone PPFRU16 Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AB021790; BAA96449.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9LUX2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. KIKUSUI; TISSUE=FRUIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrus pyrifolia (Japanese pear) (Pyrus serotina).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosida
eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPFRU16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metallothionein-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9LUX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O23812 PRELIMINARY; PRT; /4 km.
O23812;
O1-AN-1998 (TrEMBLrel. 05, Created)
O1-JAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Plant metallothionein-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: D50641: BAA23628.1; InterPro: IPR000347; Metallothion_15. Pfam: PF01439; Metallothio_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001611; Metallothion_15; 1.
SEQUENCE 74 AA; 7409 MW; F86C8CC3ED58B1C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roots."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Charyota; Waqnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                        36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A plant metallothionein-like gene from iron deficiency barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakanishi H., Okumura N., Kanegae R., Umehara Y., Nishizawa N.,
                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                              1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 IVLGVGSAKVQFE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
mes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 VILGVGPAKIQFE 13
                                                                                                                                IIVGVAPAKMFYEG 49
                                                                                                                                                                                                                                                         Similarity
       PRELIMINARY;
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NK1558;
                                                                                                                                                                                                                                                       65.7%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.7%;
69.2%;
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Last annotation update)
                                                                                                                                                                                                                                                 Score 46; D
Pred. No. 0.
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     PRT;
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                          Mismatches
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77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 AA.
                                                                                                                                                                                                                                                 DB 10; Length 75;
).99;
AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone PPFRU16.";
                                                                                                                                                                                                                        2;
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                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                           Query Match
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  Q944W1;
Q944W1;
01-DEC-2001
01-DEC-2001
01-MAR-2002
Type 2 metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Shang Y.W., Ma M., Tam F.Y., Wong Y.S.;

"Cloning and sequencing of metallothionein (MT) cDNA from a heavy

metal tolerant plant, Typha Latifolia.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF279655; AAK28022.1;

InterPro; IPR000347; Metallothion_15.

Pfam; PF01439; Metallothion_15.

ProDom; PD001611; Metallothion_15.1.
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Typhaceae; Typha
                                                                                                                                                                                                                                                                                                                                                                                                                                               Metallothionein-like protein.
Typha latifolia (Common cattail).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cork metallothionein.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ277599; CAC39481.2; -.
InterPro; IPR000347; Metallothion_15.
Pfam; PF01439; Metallothio_2; 1.
ProDom; PD001611; Metallothion_15; 1.
ProDom; PD001611; Metallothion_15; 1.
SEQUENCE 77 AA; 7673 MW; C867A295A9DAB0A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AU16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9AU16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quercus suber (Cork oak).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids I; Fagales; Fagaceae; Quercus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q93X22;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                         40 MILGVAPQKGHFEG
                                                                                                                                                                                               Local Similarity
mes 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PERIDERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                    1 VILGYGPAKIOFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 LIVGVAPQKTHFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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C-2001 (TrEMBLrel. 19, C
C-2001 (TrEMBLrel. 19, L
R-2002 (TrEMBLrel. 20, L
2 metallothionein-like p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                    79 AA;
                                                                       PRELIMINARY;
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                               Metallot\overline{h}ion_15; 1.
7954 MW; BB1C1530D3E4EC2D CRC64;
                                                                                                                                          53
                                                                                                                                                                                                         61.4%;
64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.4%;
57.1%;
            Last sequence update)
Last annotation updat
protein
                                         Created)
                                                                                                                                                                                                       Pred. No. 3
                                                                                                                                                                                                                     Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; I
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                           Mismatches
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                                                                    79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AA
                                                                                                                                                                                                                   DB 10; Length 79;
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6;
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           update)
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                                                                                                                                                                                          Indels
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OS
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Best Local :
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Magnoliophyta; Liliopsida; Poales; Typhaceae; Typha
RESULT 8
Q9SC90
Q9SC
ID Q9SC
AC Q9SC
DT 01-M
DT 01-C
DT 01-P
DE Pect
GN PER.
OS Medi
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EMBL: AF419840; AAL09705.1;

InterPro; IPR000347; Metallothion_15.

Plam; PF01139; Metallothio_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang Y.-W., Tam F.-Y., Wong Y.-S.; "Cloning and characterization of type 2 metallothionein-like gene from "Cloning and characterization of type 2 metallothionein-like gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 094187;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
putative metallothionein-like protein type 2B.
putative metallothionein-like protein type 2B.
Atropa belladonna (Belladonna) (Deadly nightshade).
Atropa belladonna (Belladonna) (Deadly nightshade).
Atropa belladonna (Belladonna) (Deadly nightshade).
Tracheophyta; Tracheophyta; Enbaryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q94187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nouar E., Baucher M., Jaziri M.;
"Differential gene expression in Atropa belladonna leafy gall.";
"Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               Universite Libre de Bruxelles, Brussels, Belgium.

EMBL; AJ30387; CAC40757.1;

InterPro, IPR000347; Metallothion_15.

Pfam; PF01439; Metallothio_2; 1.

ProDom; PD001611; Metallothion_15; 1.

PRODOM; PD001611; Metallothion_15; 1.

PRODOM; PD001611; Metallothion_15; 1.

PRODOM; PD001611; Metallothion_15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=33113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VILGVGPAKIOFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                  Thesis (2001), Department of Plant Biotechnology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                 01-MAY-2000 (TIEMBLIEL 13, Created)
01-OCT-2000 (TIEMBLIEL 15, Last sequence update)
01-MAR-2002 (TIEMBLIEL 20, Last annotation update)
Pectin methyl-esterase PER precursor (EC 3.1.1.11).
                                                                                                                     095090
 Medicago truncatula (Barrel medic)
                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                    40 LVLGVGPEKTSFD 52
                                                                                                                                                                                                                                   1 VILGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD001611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metallothion_15; 1.
8053 MW; BB090030C6F1EC2D CRC64;
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                                                                                                                                                                                                                                                                                               60.0%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                 Score 42;
pred. No.
                                                                                                                                     PRT;
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                                                                                                                                         602 AA
                                                                                                                                                                                                                                                                                                                     DB 10; Length 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best
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"MtPER, a new pectin methyl-esterase gene from Medicago truncatula
"NtPER, a new pectin methyl-esterase of root nodules by the symbiotic
involved in the infection process of root nodules by the symbiotic
host Sinorhizobium meliloti.";
host Sinorhizobium meliloti.";
spimitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3880;
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밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nodule development.";
submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJZ49611; CAB65290.2;
InterPro; IPR0000070; Pectinesterase.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR003880; Ppantne_attach.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01095; Pectinesterase; 1.; 1.
PROSITE; PS00800; PECTINESTERASE 1; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                             Matches
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           082562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elaeagnus umbellata (Autumn Olive).
Elaeagnus umbellata (Autumn Olive).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Elaeagnatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
Spermatophyta; Magnoliophyta; eudicotyledons.
eurosids I; Rosales; Elaeagnaceae; Elaeagnus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 IIGDGPAKTKFTG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          082562
                                                                                                                                                                                                                                                                                                             Kim H.B., An C.S.;

"Isolation and characterization of cDNA clone encoding metallothionein "Isolation and characterization of cDNA clone encoding metallothionein from the root nodule of Elaeagnus umbellata.";

from the root nodule of Elaeagnus umbellata.";

submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF091514; AEC62105-1;

EMBL; AF091514; Metallothion_15.

Pfam; PF01439; Metallothion_15;

ProDom; PD001511; Metallothion_15;

Proprodom; PD001511; Metallo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=43233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                  SEQUENCE
31 VLGVAPEKGNFEG 43
                                                                                                                                                                            Local
                                                                  2 ILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JEMALONG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 36 E
602 AA; 65003 MW;
                                                                                                                                                    8;
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                 69 AA;
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodriguez-LLorente I.D., Kondorosi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.0%;
                                                                                                                                                                                                                                                                                                         7141 MW;
                                                                                                                                                                                                       58.6%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pred.
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                                                                                                                                                                                                       Score 41; I
pred. No. 7.

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 602;
                                                                                                                                                                                                                                                      DB 10; Length 69;
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                                                                                                                                                                                                               0;
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RESULT 12
006352
                                                                                                                                                             Best Local Similarity Matches 7; Conserv
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            006352
                                                                                                                                                        Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018705; AAH18705.1; ...
Interpro; IPR001392; Clathrn_med.
Pfam; PF00928; Adap_comp_sub; 1.
                                                             400 LGLGPASLSFE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 50, 0 protein.
Homo sapiens (Human).
                                                                                                                                                                                                                          Strausberg R.;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                  3 LGVGPAKIQFE 13
                                                                                                                                                                                                                                                                                                                                                                             28WV65
                                                                                                                                                                                                                                                                                                                                                                   Q8WV65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF201384; AAG39645.1; ... InterPro; IPR000347; Metallothion_15. Pf1139; Metallothio_2; 1. ProDom; PD001611; Metallothion_15; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            40 LILGVGPEKTSF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and characterization of cDNAs for metallothionein-like protein from Petunia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-PETUNIA MULTIFLORA HYBRID, AND CV. PRIMETIME ROSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Petunia hybrida (Petunia).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9FR40
PRELIMINARY; PRT; 80 AA.
O9FR40;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VILGVGPAKIQF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tecar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
      PRELIMINARY;
                                                                                                                                                     453 AA;
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                       49977 MW; AE3DCA8C5AED08B7 CRC64;
                                                                                                                  63.6%;
                                                                                                          58.6%; Score 41; DB 63.6%; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%;
66.7%;
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4248ADE0C05FACC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
54 AA.
                                                                                                                                                                                                                                                                                                                                                                453 AA.
                                                                                                                DB 4; Length 453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10; Length 80;
                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                          0;
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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В

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OS OC OC OC OC OX RN RP RC RX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RX MEDINE-98395987; PubMed-9634230;
RA COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Rutter S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
RT Complete genome sequence.";
RRI Nature 393:537-544(1998).
                                                                                                                                               MEDLINE=98267202; PubMed=9602134;
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                01-NOV-1998 (TIEMBLIEL 08, Created)
01-NOV-1998 (TIEMBLIEL 08, Last sequence update)
01-MAR-2002 (TIEMBLIEL 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                 080335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; CompleseQUENCE 54 AA; 5695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.",
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; 295390; CAB08712.1;
EMBL; AE007162; AAR47952.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TubercuList; Rv3489; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-CDC 1551 / OSHKOSH;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

KOlonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,

Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                       44 MLGIGPAKLE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ILGVGPAKIQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    006352;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Rv3489, Last annotation update)
RV3489 OR MTCY13E12.42 OR MT3593.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               57.1%; Score 40; DB 16; Length 54; 60.0%; Pred. No. 8.5; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
95 MW; 3406A9C3DF1FBC96 CRC64;
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                            79 AA.
                                                                                                                                                               core eudicots; Rosidae;
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RESULT 14
Q94198
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ID Q92R3
AC Q92R3
DT 01-DE
DT 01-DE
DT 01-MA
DE HYPOT
GN R01108
OS Rhizc
OC Rhizc
OC Rhizc
OC RDIZ
RN [1]
RP SEQUE
RC STRAJ
RX MEDLJ
RA Capal
RA GOdri
RA GOdri
RA Pohia
RA ROMA
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                   Q92R37 PRELIMINARY;
Q92R37;
Q92R37;
Q1-DEC-2001 (TrEMBLrel. 19, Cr
Q1-DEC-2001 (TrEMBLrel. 20, La
Q1-MAR-2002 (TrEMBLrel. 20, La
Hypothetical protein R01087.
R01087 OR SMC02636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000347; Metallothion_15. pfam; PF011439; Metallothio_2; 1. probom; PD001611; Metallothion_15; 1. SEQUENCE 79 AA; 7741 MW; CDDAE5CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 211:221-227(1998).
EMBL; AB008100; BAA31561.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q94198 PRELIMINARY; PRT; 82 AA.
Q94198.
01-DEC-2001 (TremBLrel. 19, Created)
01-DEC-2001 (TremBLrel. 19, Last sequence update)
01-JUN-2002 (TremBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atropa belladonna (Belladonna) (Deadly nightshade).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Atropa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methallothioneine-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-21396507; PubMed-11481430;
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Botsard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
                                                                                                                                                                        Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=33113;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                              Rhizobiaceae; Sinorhizobium.
                                                                                                                                             NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 LVLGVAPVKMHSEG 55
                                                                                                                                                                                                                                                                                                                                                                  41 LVLGVGPEKTSF 52
                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity les 7; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VILGVGPAKIQFEG 14
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58.3%;
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                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40;
Pred. No.
                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                201 AA.
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Search completed: January 13, 2003, 09:59:42 Job time : 56.1282 secs
                                                               B
                                                                                            Ω
                                                                                                                               Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                          Sinorhizobium meliloti strain 1021.";
proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591786; CAC45666.1; -.
Hypothetical protecin; Complete proteome.
SEQUENCE 201 AA; 21985 MW; 6610A10C3F5DDCB4 CRC64;
                                                                                                                            Local Similarity les 7; Conserv
                                                                 63 IGVGKAGLEFEG 74
                                                                                               3 LGYGPAKIQFEG 14
                                                                                                                              Conservative
                                                                                                                                                57.1%;
58.3%;
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                                                                                                                                                Score 40; DB Pred. No. 33;
                                                                                                                                    Mismatches
                                                                                                                                                                 16; Length 201;
                                                                                                                                    2;
                                                                                                                                        Indels
                                                                                                                                      0
                                                                                                                                      Gaps
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OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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   WS-08-969-683A-35
WS-08-968-917A-4
US-09-618-192A-319
WS-09-615-192A-319
WS-09-615-192A-319
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WS-09-316-987A-10
US-08-370-700-10
WS-08-93-228-12
US-08-93-228-12
US-08-93-165A-458
US-08-93-165A-458
US-08-785-795-5
US-08-785-795-7
US-09-651-941-7
US-09-651-941-7
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US-09-651-941-7
US-09-650-3-91-84
US-07-754-918A-14
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US-09-134-001C-3689
US-08-724-354D-4
                                                                                                                                                                                                                                                                                                              US-08-322-962-5

US-08-450-653-5

US-08-491-522-7

US-09-491-522-1

US-09-491-522-5

US-09-968-563-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                    Sequence 5, Appli
Sequence 5, Appli
Sequence 7, Appli
Sequence 11, Appli
Sequence 5, Appli
                                                                                                                                             Sequence 35, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 72, Appl
Sequence 319, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 2, Appli
Sequence 458, Appli
Sequence 458, Appli
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Sequence
Sequence
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Sequence
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                 Sequence 4, Appli
                                             Sequence
                                              e 8, Appli
e 14, Appl
e 3689, Ap
                                                                                      7, Appli
7, Appli
                                4023,
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228 320 321 323 334 335 336 337 34 34 34 34 34 34 34 34 34 34 34 34 34
33 32 32 33 34 34 34 34 34 34 34 34 34 34 34 34
48.6 48.6 47.9 47.1 47.1 47.1 47.1 47.1 47.1 47.1 47.1
1043 1118 1118 1118 28 311 311 361 361 363 365 365 365 365 365 365 365 365
1414811411481184141
US-09-270-984A-4 US-08-724-354D-2 US-09-270-984A-2 US-07-945-283-2 US-08-427-072-9 US-08-118-270-37 PCT-US-30-08528-37 PCT-US-30-162-4 US-08-685-945B-4 US-08-685-945B-2 US-08-685-945B-2 US-08-155-005A-8 US-08-186-756A-4 US-08-880-865-4 US-08-416-756A-3
Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 37, Appli Sequence 37, Appli Sequence 4857, Ap Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1, Appli Sequence 3, Appli Sequence 4, Appli Sequence 3, Appli

### ALIGNMENTS

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RESULT 1
US-08-322-962-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 5, Application US/08322962 patent No. 5466785
OTHER INFORMATION:
OTHER INFORMATION:
US-08-322-962-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Tissue-Preferential Promoters NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                               TELEFAX: 919-541-8009
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30B
SOPTWARE: PatentIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/071,209
FILING DATE: 02-JUN-1993
                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 0
APPLICATION NUMBER: 12-APR-1990
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                        FEATURE:
                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/322,962
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                       LENGTH: 75 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                              TOPOLOGY:
                                                          LOCATION:
                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                  919-541-8689
                                                                                                                                linear
                                                                               protein
                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                               US 07/508,207
                              /note= "Protein product of pea
metallothionein reported by Evans et al."
                                                                                                                                                                                                                                                                                                        32,943
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Matches

STATE:

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; Sequence 7, Application US/09491522
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                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08450653 Patent No. 6018099
                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                    36 VILGVGPAKIQFEG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "Protein product of pea
OTHER INFORMATION: metallothionein reported by Evans et al."
                                                                                                                                   1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      Local Similarity es 14; Conserv
                                                                                                                                                                                                                                                                                           NAME/KEY: Protein LOCATION: 1.75
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DeFramond, Annick J
TITLE OF INVENTION: Tissue-Pref
NUMBER OF SEQUENCES: 13
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Clan Company: 7 Skyline Drive
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linear
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                                                                                                                                                                100.0%; Score 70; DB 3; Length 75; 100.0%; Pred. No. 1e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue-Preferential Promoters
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100.0%; Pred. No. 1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                  5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 75;
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                                                                                                                                                                  0;
                                                                                                                                                                Gaps
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                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                       US-09-491-522-11
                                                                                                                                                                                                                                                                            ; Sequence 11, patent No. 6
                                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: US-09-491-522-7
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
               COMPUTER READABLE FORM.
MEDIUM TYPE: Diskette
                                                                                                                                     APPLICANT: COlige, Alain
APPLICANT: Lapiere, Charles M.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent NO. . . GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
COlige, Alain
APPLICANT: Colige, Alain
APPLICANT: Lapiere, Charles M.
APPLICANT: Lapiere, Charles M.
FAPPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: RECOMBINANT N-PROTEINASE,
AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Abrams Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-935
TELEFAX: 650-493-5556
                                                                                 STREET: LL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6428998
GENERAL INFORMATION:
                                                 COUNTRY: USA
ZIP: 10036-2811
        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                               270 VLLGVDDSVVQFHG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NY
COUNTRY: USA
2IP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                        ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 566 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                             1, Application US/09491522
6428998
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                       52.9%; Score 37; 50.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Windows
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 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 566;
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US-09-491-522-7

RESULT 3

В

US-08-450-653-5

FEATURE:

LENGTH:

0; Gaps

0;

Matches Query Match

# us-09-554-941-1.rai

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US-09-491-522-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPEKATING SYSTEM: Windows
SOFTMARE: FRASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence 5, Application US/09491522 patent No. 6428998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Abrams, Samuel REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Colige, Alain
APPLICANT: Laptere, Charles M.
APPLICANT: Laptere, Charles M.
APPLICANT: Laptere, Charles M.
APPLICANT: Prockop, Darwin J.
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
TITLE OF INVENTION: AND THE PRODUCTION, METHODS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 VLLGVDDSVVQFHG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                        OPERATING SYSTEM: Windows Version SOFTWARE: FASTSEO for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VILGYGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/886,333
                                                                                                                                                                                                                                                                                                                                                 CITY:
STATE:
                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 650-493-4935
                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                           APPLICATION NUMBER: US/09/491,522
                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                 FILING DATE:
                                                                         NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 838
                                                                                                                                                                                                                                                                                                                     10036-2811
                                                                                                                                                                                                                                                                                                                                                                  New York
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                                                                                                                                                                                                                                                                                                                                                                               3: Pennie & Edmonds, LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                       USA
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Pred. No. 1.8e+02;
Pred. No. 1.8e+02;
Mismatches 4; Indels
                                                                                        8389-0060-999
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SEQUENCE CHARACTERISTICS:
LENGTH: 1211 amino acids
TYPP: amino acid
STRANDENCESS: single
TOPOLOGY: linear
US-09-491-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: RAMESCH V. NAIR
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VILGVGPAKIQFEG 14
                                                                                                               APPLICATION NUMBER: 60/030,601
APPLICATION NOVEMBER 13, 1996
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOVD, LINDA AXAMETHY
NAME: FLOVD, LINDA AXAMETHY
RECISTRATION NUMBER: CR-9982
RECISTRATION NUMBER: CR-9982
REFERENCE/DOCKET NUMBER: CR-9982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                      TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/968,563
                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                       FILING DATE:
LENGTH: 194 amino acid TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6013494
                                                                                                                                                                                                                                                                                                                                                                          : ROCHESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08968563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WILMINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARLES E. NAKAMURA
ANTHONY A. GATENBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GREGORY M. WHITED
VASANTHA NAGARAJAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMY (KUANG-HUA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DONALD E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MARIA DIAZ-TORRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHARON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICHARD D. LA REAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STEPHEN K. PICATAGGIO RAMESCH V. NAIR
                                  194 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAYNE
         unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 4;
pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 1211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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US-08-969-683A-35
                                               Matches
                                                                     Query Match
                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/20873
PILING DATE: 13-NOV-1997
PILING DATE: 13-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 NAME: Glaister, Debra REGISTRATION NUMBER: 33,888 REFERENCE/DOCKET NUMBER: GC 3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-864-620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-969-683A-35
                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 35, Application US/08969683A Patent No. 6136576
GENERAL INFORMATION:
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30 VVIGVGPA 37
                                                    Local Similarity
                     1 VILGVGPA 8
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                              TELEPHONE:
TELEFAX: 6
                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Windows
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                                                                                    ORGANISM:
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/969,683A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genencor International, Inc. STREET: 4 Cambridge Place
STREET: 1870 South Winton road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: prote ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 VVIGVGPA 37
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                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                       14618
                                                                                                                                                           194 amino acids
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rochester
                                                                                                                                                                                                            650-845-6504
                                                                                                   DHAB2
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WETHOD FOR THE RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                           Diskette
                                          51.4%; Score 36; DB 75.0%; Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRODUCTION OF 1,3 PROPANEDIOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.48;
75.0%;
                                2; Mismatches
                                                                                                                                                                                                                                          GC 369-2
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                DB 4; Length 194;
                           0; Indels
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                          0;
                      Gaps
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SEQUENCE DESCRIPTION: SEQ ID NO: 72: non-cyanogenic strand-glucosidase precu
            Query Match
Best Local Similarity 53.8%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches
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Sequence 72, Application US/08914375C;
Patent No. 6377893

GENERAL INFORMATION:
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                                                                                                                                                                                                             TELEFAX: 352 331 0462
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                            COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
APPLICATION UNBER: US/08/914,375C
FILING DATE: 19-Aug-1997
CLASSIFICATION INFORMATION:
TELEPHONE: 352 392 7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local (
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APPLICANT: Campisi, Judith
APPLICANT: Kim, Sahn-Ho
TITLE OF INVENTION: TRFI B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09608917A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/608,917A
CURRENT FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE:
                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
ORIGINAL SOURCE:
                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GVGPAKIQF 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GVGPASLRF 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Steven A. Benner
Applications of Protein Structure Predictions
NUMBER OF SEQUENCES: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                    OTHER INFORMATION:
                                                                                                                           ORGANISM: Trifolium repens
                                                                                                                                                                                                      LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Steven A. Benner
STREET: 1501 NW 68th Terrace
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Regents of the University of California
                                                                                                                                                                                                                                                                                                                                                                                                               32605-4147
                                                                                                                                                                                                                                                                                                                                                                                                                     United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N: TRF1 Binding Protein
LBNL IB 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.4%; Score 36; DB 66.7%; Pred. No. 88;

 Mismatches

                                 DB 4; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 414;
             5
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       0,
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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0,
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DB 4; Length 141;

0

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US-09-063-035-2

sequence 2, Application US/09063035 Patent No. 6160091

INFORMATION:

PEUKERT, Karen; HAENEL, Frank; and EILERS, Martin

APPLICANT:
APPLICANT:

0;

Š US-09-063-035-2 FILE REFERENCE: 11000.1003c400
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR PRIOR DATE: 1996-09-11 US-09-615-192A-319 ; TYPE: PRT; ORGANISM: Eucalyptus grandis US-09-615-192A-319 Sequence 319, Application US/09615192A Patent No. 6410718 GENERAL INFORMATION: Best Local Similarity
Matches 6; Conserva Query Match CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: MEDIUM TYPE: Diskette, 3.5 inch, 1.2 mb storage COMPUTER: IBM AT-compatible, 80486 processor OPERATING SYSTEM: MS-DOS version 6.1 SOFTWARE: Wordberfect version 8.0 CURRENT APPLICATION DATA: TITLE OF INVENTION: Myc-binding zinc finger proteins, TITLE OF INVENTION: their preparation and their use SOFTWARE: FO CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of plant Lignin Content APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka NUMBER OF SEQUENCES: COMPUTER READABLE FORM: PRIOR APPLICATION NUMBER: US OF PRIOR FILING DATE: 1998-10-09 NUMBER OF SEQ ID NOS: 405 COUNTRY: STATE: CITY: Washington STREET: ADDRESSEE: 244 GAGPAEVKEEG 254 LENGTH: 803 amino acids Type: amino acid TopoLOGY: linear APPLICATION NUMBER: FILING DATE: 21-APP LENGTH: 4 GVGPAKIQFEG 14 20036 D.C. 141 E: Keil & Weinkauf 1101 Connecticut Avenue SEQ ID NOS: 405 FastSEQ for Windows Version 3.0 USA Conservative 21-APR-1998 1996-09-11 UMBER: US 09/169,789 54.5%; US/09/063,035 Score 36; DB 4; pred. No. 1.8e+02; pred. No. 1.8e+02; Indels Length 803;

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US-08-948-564-12 protein
                                                                                                                             TELEFAX: 919-854-14-01
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                 Matches
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-948-564-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LENGTH: 395
; TYPE: PRT
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08948564 Patent No. 6121512 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Treadway, Patti J
APPLICANT: Turner, Jan R
PAPLICANT: Waldron, Clive
TITLE OF INVENTION: Blosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
EARLIER APPLICATION NUMBER: US/09/370,700
EARLIER APPLICATION NUMBER: US/09/36987
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0

LENCHIP OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Siminzsky, Balazs
APPLICANT: Dewey, Ralph E.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: PO Box 37428
                                                                                                                                                                                           TELEPHONE: 915-CT TD NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Crawford, Kathryn P
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: PU CAN CITY: Raleigh
CTTY: Raleigh
CTATE: No. 6121512th Carolina
                            Local Similarity es 6; Conserv
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 GAGPAKLQ 27
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                    Conservative
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     50.0%; Score 35; DB 3; Length 516
50.0%; Pred. No. 1.7e+02;
ative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                          800
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75.0%;
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                                       DB 3; Length 516;
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Gaps
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Search completed: January 13, 2003, 09:56:22 Job time: 14.2051 secs
                                                                            밁
                                                                                                                                                                                               APPLICANT: Cunningham Jr, Francis X
APPLICANT: DellaPenna, Dean
TITLE OF INVENTION: Method for Regulating Carotenoid Biosynthesis in
FILE OF INVENTION: Marigolds
FILE REFERENCE: Quest 41-162
CURRENT APPLICATION NUMBER: US/09/201,641A
CURRENT FILING DATE: 1988-11-30
NUMBER OF SEQ ID MOS: 8
SOFTWARE: Patentin Ver. 2.0
LENGTH: 516
TYPE: PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-201-641-6
                                                                                                                                           Query Match
Best Local Similarity 42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qγ
                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09201641A PATENT NO. 6232530 GENERAL INFORMATION:
                                                              98 VVIGCGPAGLALAG 111
                                                                                             1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 LFVGPRKLSYDG 110
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ف
                                                                                                                             Conservative

 Mismatches

                                                                                                               Score 35; DB 4; ....
Pred. No. 1.7e+02; ....
                                                                                                                                                 DB 4; Length 516;
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                                                                                                              Gaps
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OM protein - protein search, using sw model
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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published_Applications_AA:*

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14: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                January 13, 2003, 09:54:16; Search time 64.9744 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118974 seqs, 19401057 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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4.180 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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969 10 366 10 467 9 510 9 517 77 1 70 1 1221 1 125 1 135 9 135 9 359 359 359 359 359	ength DB
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US-09-321-987B-5 US-09-31-368-254-6965 US-09-738-626-5777 US-09-738-626-5777 US-09-739-98D-54 US-09-899-887-279 US-09-939-980-458 US-09-764-887-279 US-09-764-887-279 US-09-764-887-279 US-09-783-263-203 US-09-833-263-203 US-09-978-2586-45 US-09-978-192A-45 US-09-978-192A-45 US-09-978-192A-45 US-09-978-192A-45 US-09-978-192A-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-193-45 US-09-978-189-45 US-09-978-189-45	D TIS-09-864-761-36875
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App Ap Ap Appl Appli Appl Appl Appl Appl	5, A ppli

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48.6 48.6 48.6 48.6 48.6 48.6 48.6 48.6
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333772 30772 30772
See
sequence 1 sequence 1 sequence 6 sequence 6 sequence 6 sequence 5 sequence 5 sequence 5 sequence 5 sequence 5 sequence
quence 1003 quence 13900 quence 6755, quence 6296, quence 6393, quence 5817, squence 5817, squence 1016 equence 1016 equence 132 equence 132 equence 130 sequence 130 sequence 6, sequence 5, sequence 5, sequence 5, sequence 5, sequence 50, sequence 51, sequence 51, sequence 51, sequence 31,
equence 10037, A equence 13900, A sequence 11208, A sequence 6755, Ap squence 6393, Ap squence 4369, Ap equence 5817, Ap sequence 23, App1 sequence 11807, Ap sequence 11807, Ap sequence 1327, Ap sequence 13702, A sequence 13702, A sequence 13702, A sequence 14017, A sequence 14017, A sequence 17017, A sequence 5, App11 sequence 6, App11 sequence 10943, A sequence 1588, Ap sequence 4706, Ap sequence 4706, Ap sequence 3775, A
Sequence 10037, A Sequence 13900, A Sequence 6755, Ap sequence 6393, Ap sequence 4399, Ap sequence 3391, Ap Sequence 32, Appl Sequence 32, Appl Sequence 11887, A Sequence 13027, A Sequence 13027, A Sequence 13021, A Sequence 10021, A Sequence 10023, Appli Sequence 10043, A Sequence 10043, A Sequence 3, Appli Sequence 4706, Ap Sequence 3708, Ap Sequence

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; Sequence 36875, Application US/09864761
; Patent NO. US20020048763A1
; GENERAL INFORMATION:
TITLE OF INVENTION COMPARE TO THE REFERENCE: ACONGEST TO SO THE TOTAL TO THE TELL OF THE T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO APPLICANT: Chen, Wensheng GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR APPLICANT: Chen, Wensheng GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENOME-DERIVED ANALYSIS BY MICROARRAY
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APPLICANT: Kimble, Judith E
APPLICANT: Blelloch, Robert H
FILE REFERENCE: 960296,95386
CURRENT APPLICATION NUMBER: US/09/321,987B
PRIOR APPLICATION NUMBER: US/09/321,987B
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR APPLICATION NUMBER: 60/087,170
PRIOR APPLICATION NUMBER: 60/129,023
VENTOR APPLICATION NUMBER: 60/129,023
SOFTWARE: 1999-04-13
SOFTWARE: PATENTIANE DATE: 1999-04-13
SOFTWARE: PATENTIANE: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 969
TYPE: PRT
ORGANISM: Bovine
US-09-321-987B-5
                                                                               US-09-801-368-254
                                                                                                                                                                                                                                                         B
                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO AL049539.19
OTHER INFORMATION: EXPRESSED IN BY144, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN HALNO, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELACINTA, SIGNAL = 3.3
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US-09-864-761-36875
                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-321-987B-5
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Patent No. US20020102210A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                  1 VILGVGPAKIOFEG 14
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 52.9%; Score 37; DB 50.0%; Pred. No. 87;
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254, Application US/09801368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VLAVGPAQLQAE 18
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les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                        Mismatches

 Mismatches

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                                                                                                                                                                                                                                                                                                                    4; Indels
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
PRIOR APPLICATION NUMBER: D9/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER: OF SEQ ID NOS: 7059
SEQ ID NO 6965
IFMCTHI. ACT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6965
                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-738-626-6965
                                    LENGTH: 467
TYPE: PRT
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APPLICANT:
APPLICANT:
APPLICANT:
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ADDITIONAL ADDITION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Saccharomyces cerevisiae US-09-801-368-254
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SED ID NOS: 440
                                                                                                                                                                                                                                                            APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
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APPLICANT: MIZOGUCHI, HIROS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 VMAVMPPEVQFDG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               es 5; Conserv
                                                                                                                                                                                                                                                                            YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                  IKEDA, MASATO
                                                                                                                                                                                                                                                                                                     HAYASHI, MIKIRO
OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Royer, John
Salama, Sofie
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Milne, Todd
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                                                                                                                                                                                                                                                                                                                                    SEIKO
                                                                                                                                                                                                                                                                                                                                               HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%; Score 35; DB 38.5%; Pred. No. 63;
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US-09-738-626-5777
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR TILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEO ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-323-998D-54
              CURRENT APPLICATION NUMBER: US/09/323,998D
CURRENT FILING DATE: 1999-06-02
PRIOR APPLICATION NUMBER: 09/088,724
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 09/088,725
PRIOR APPLICATION NUMBER: 09/087,715
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR APPLICATION NUMBER: 08/937,155
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR APPLICATION NUMBER: 08/624,125
PRIOR FILING DATE: 1996-03-29
NUMBER: 05/09-25
PRIOR FILING DATE: 1996-03-29
NUMBER: 05/09-25
PRIOR FILING DATE: 1996-03-29
NUMBER: 05/09-25
PRIOR FILING DATE: 1996-03-29
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Best Local Similarity
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SEQ ID NO 5777
LENGTH: 510
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKTHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CUNNINGHAM JR., FRANCIS X.
APPLICANT: SUN, ZAIREN
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/09323998D Patent No. US20020102631A1
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Best Local :
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APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENES OF CAROTENOID BIOSYNTHESIS AND METABOLISM AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REFERENCE: 108172-09019
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 VVVGAGPTGVELAG 185
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35.7%;
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US-09-323-998D-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus Subtilis US-09-899-482-2
                                                                                                                                                                                                                                                                                                                                                                           US-09-939-980-458
Sequence 458, Application US/09939980
Patent No. US20020082234A1
GENERAL INFORMATION:
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Best Local Similarity 42.9%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09899482 Patent No. US20020006641A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: EP 97305286.3
PRIOR FILING DATE: 1997-07-16
PRIOR APPLICATION NUMBER: EP 97305344.0
PRIOR FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: Increasing Production of Proteins in Microorganisms
FILE REFERENCE: GC385-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/899,482
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ILGYGPAKIQFEG 14
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                      TITLE OF INVENTION: NO. US20020082234Alel Prokaryotic Polynucleotides, Polypeptides and Their Uses
                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                    NUMBER OF SEQUENCES: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737
                                                      COUNTRY: USA
                                                                      STATE: PA
                                                                                     CITY: King of Prussia
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                                                                                                                                                                                                                                                         Lonetto, Michael
Nicholas, Richard
Pratt, Julie
                                                                                                                                                                                                                                                                                                                                                               Black, Michael
                                                                                                                                                                                                        Rosenberg, Martin
Ward, Judith
                                                                                                                                                                                                                                                                                                                           Hodgson, John
                                                                                                                                                                                                                                       Reichard, Richard
                                                                                                                                                                                                                                                                                                            Knowles, David
                                                                                                                                                                                                                                                                                                                                              Burnham,
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    Mismatches

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RESULT 10
US-09-764-887-279
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US-09-764-884-30
US-09-764-884-30
; Sequence 30. Application US/09764884
; Patent No. US20020161208A1
                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-764-884-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; SEQUENCE DESCRIPTION: SEQ ID NO: 458: US-09-939-980-458
                                                  Sequence 279, Application US/09764887 Patent No. US20020042096A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 30
LENGTH: 121
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT2/03
CURRENT APPLICATION NUMBER: US/09/764,884
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                        Query Match
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 458:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
                                                                                                                                                                              96 VIGIAQGKIVFDG 108
                                                                                                                                                                                                                                             48.6%;
Local Similarity 38.5%;
les 5; Conservation
                                                                                                                                                                                                                2 ILGVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 GVGPNKENFE 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/936,165
FILING DATE: CURKNOWN>
ATTORNEY_AGGENT INFORMATION:
    NAME: Gimmi, Edward R
    REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.6%;
                                                                                                                                                                                                                                                                   Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 10; Length 70; Pred. No. 13;
                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                 DB 9; Length 121; 26;
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; Sequence 203, Application US/09922217
; Patent No. US20020076414A1
                               US-09-922-217-203
                                               RESULT 12
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                                                                                                                                                                                                                                                  SEQ ID NO 203
LENGTH: 135
TYPE: PRT
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Best Local Similarity
6; Conserve
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                                                                                                                                                             Matches
                                                                                                                                                                                         Query Match
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LENGTH: 125
                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/025,380 CURRENT FILING DATE: 2001-12-19
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APPLICANT:
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/764,887 CURRENT FILING DATE: 2001-01-17
                                                                                              80 GVNPGKLDVEG 90
                                                                                                                                                           Local Similarity
les 6; Conserv
                                                                                                                          4 GVGPAKIQFEG 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 LGMGPGKAEPQG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A. W. Fanger, Gary R. Vedvick Thomas S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clapper,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Aijun
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Smith, Carole L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes, Michael J
                                                                                                                                                        Conservative
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                                                                                                                                                                        48.6%;
54.5%;
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                                                                                                                                                        1; Mismatches
                                                                                                                                                                        Score 34; DB Pred. No. 29;
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                                                                                                                                                                                    9; Length 135;
                                                                                                                                                      Indels
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michae

APPLICANT: APPLICANT:

Meagher, Madeleine Joy Secrist, Heather Benson, Darin R. Lodes, Michael J.

APPLICANT:

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; ORGANISM: Homo sapiens US-09-922-217-203
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US-09-833-263-203
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SEQ ID NO 203
LENGTH: 135
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                        RESULT 14
US-09-978-295A-45
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Best Local Similarity
Conserv
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CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 203
LENGTH: 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 203, Application US/09833263 Patent No. US20020110547A1
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TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Aijun
APPLICANT: Clapper, JC
APPLICANT: Stolk, Johr
APPLICANT: Meagher, Ma
                                                                                                                                        sequence 45, Application US/09978295A Patent No. US20020156006A1
                                                                                                                          GENERAL INFORMATION:
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                                                        APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, Davi
APPLICANT: Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                              APPLICANT:
 APPLICANT:
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Local Similarity 54.5%;
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Smith, Carole Lynn
King, Gordon E.
Wang, Aijun
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Ferrara, Napol
Filvaroff, Ell
Fong, Sherman
                                                Eaton, Dan
                                                            Desnoyers, Luc
                                                                             Botstein, David
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                    , Napoleon
ff, Ellen
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pred. No. 29;
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Pred. No. 29;
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PRIOR APPLICATION NUMBER: 09/063250
PRIOR APPLICATION NUMBER: 09/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PRILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/064249
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-3
PRIOR FILING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/0670450
PRIOR APPLICATION NUMBER: 60/077450
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR APPLICATION NUMBER: 60/079294
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILLING DATE: 1998-03-25
PRIOR FILLING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR APPLICATION NUMBER: 60/078886
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
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                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
                                                                                                                          PRIOR PRIOR
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                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 03-27
PRIOR APPLICATION 1000-03-27
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
                  FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/
FILING DATE: 1998-03-30
                                                                                FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920
                                                                                                                       APPLICATION NUMBER: 60/079786
                                                                                                                                                                                                               FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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Gurney, Austin L.
Hillan, Kenneth J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goddard
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PRIOR FILING DATE: 1998-04-29
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APPLICANT: Ashkenaz
APPLICANT: Baker K
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PRIOR FILING DATE: 1998-05-13
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FILING DATE: 1998-04-30
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                                                         Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Gurney, Austin L.
          Godowski, Paul J.
Grimaldi, J. Christopher
                                                                                                                             Ferrara, Na
Filvaroff,
                                              Goddard, Audrey
                                                                                                                                                            Eaton, Dan
                                                                                                                                                                                           Baker Kevin P.
Botstein, David
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ff, Ellen
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PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/0
PRIOR FILING DATE: 1998-03-10
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
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Kljavin, Ivar J.
Kuo, Sophia S.
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OR APPLICATION NUMBER: 60/082797
OR APPLICATION NUMBER: 60/082796 DR APPLICATION NUMBER: 60/083495
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083496
DR FILING DATE: 1998-04-29
DR APPLICATION NUMBER: 60/083499
DR FILING DATE: 1998-04-29
DR FILING DATE: 1998-04-29 OR FILING DATE: 1998-04-29

OR APPLICATION NUMBER: 60/08354

DR FILLNG DATE: 1998-04-29

OR APPLICATION NUMBER: 60/083558

OR FILING DATE: 1998-04-29

OR FILING DATE: 1998-04-29

OR FILING DATE: 1998-04-29

OR FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081817 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/(FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/0 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/080333 APPLICATION NUMBER: 60/080328 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 FILING DATE: APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-08 APPLICATION NUMBER: FILING DATE: 1998-04-08 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: FILING DATE: 1998-04-01 FILING DATE: 1998-04-05
APPLICATION NUMBER: 60/084366
APPLICATION 1998-05-05
APPLICATE: 1998-05-07-084414 APPLICATION NUMBER: 60/083500 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083742 FILING DATE: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-04-09 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/081203 FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084441 APPLICATION NUMBER: 60/083545 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 FILING DATE: 1998-04-APPLICATION NUMBER: 60/083322 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/082804 1998-04-01 1998-04-01 1998-04-09 1998-04-2 1998-04-15 1998-04-60/081070 60/081229 60/081049 60/080334 60/081952 60/081819 60/081195 60/081071

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| PRIOR PILING DATE: 1998-05-06
| PRIOR PILING DATE: 1998-05-07
| PRIOR APPLICATION NUMBER: 60/084639
| PRIOR APPLICATION NUMBER: 60/084640
| PRIOR PILING DATE: 1998-05-07
| PRIOR PILING DATE: 1999-05-13
| PRIOR PILING DATE: 1999-05-15
| PRIOR PILING DAT
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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4.180 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score		Length DB	10	ID 	Description Sequence 47113, A
1	41	56.2	) 49 505	10	US-09-864-761-47113	
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o	39	53.4	484	5	12 00 300 010 E0	sequence 2, Appl
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12	. 36	49.0	, (	5	15-00-005-335-6	Sequence 6, Appl
13	36	49.3	3/4	ú	CO-CO 000 EEU 0	Sequence 5433,
14	36	49.3	407	٧	US-09-/38-626-0#00	Seguence 2. Appl
5	35.5	48.6	639	10	DS-09-787-90-2	ا د
10	5	48.6	639	10	US-09-782-906-3	A (
17	35.5	48.6	639	10	US-09-782-906-4	sequence 5. Appl
18	35.5	48.6	639	10	US-09-782-906-5	Sequence 30,
19	35	47.9	86	10	08-04-88/-100-30	

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Sequence 584, Appli sequence 3, Appli sequence 3, Appli sequence 3, Appli sequence 2, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli sequence 4, Appli sequence 4, Appli sequence 2, Appli sequence 315, App sequence 48176, A sequence 4910, A sequence 4910, A sequence 35131, A sequence 35131, A sequence 3175, App sequence 4018, Appli sequence 4018, Appli sequence 310, Appli sequence 4018, Appli sequence 4018, Appli sequence 4018, Appli sequence 4014, Appli sequence 4014, Appli sequence 454, Appli sequence 56, Appli sequence 56, Appli sequence 50, Appli sequence 454, Appli seque	848

## ALIGNMENTS

PRIOR	PRIOR	RESULT 1 US-09-86 ; Sequenc ; Sequenc ; Patent ; GENERAL ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; APPLIC ; TITLE ; TITLE ; FILE ; FILE ; FILE ; FRICR PRIOR PRIOR ; PRIOR PRIOR ; PRIOR ; PRIOR
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NUMBER: PCT/US01/00665 2001-01-30 NUMBER: PCT/US01/00668 2001-01-30 NUMBER: PCT/US01/00663 2001-01-30 NUMBER: PCT/US01/00662 2001-01-30 NUMBER: PCT/US01/00662 2001-01-30 NUMBER: PCT/US01/00661	NUMBER: GB 24263.6  1 2000-10-04  NUMBER: US 60/236,359  1 2000-09-27  1 2001-01-30  NUMBER: PCT/US01/00666  2 2001-01-30  NUMBER: PCT/US01/00664  2 2001-01-30  NUMBER: PCT/US01/00664  1 2001-01-30  NUMBER: PCT/US01/00664	cation US/09864761 763A1 763A1 763A1 763A1  Prion G. Frion G. Frio
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RESULT 3
US-09-729-674-160
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                                                                                                   GENERAL
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US-09-893-737-324
                                                                                       Sequence 160, Application US/09729674
Patent No. US20010039335A1
GENERAL INFORMATION:
                         APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: LaVallie, Edward R.
   APPLICANT:
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 324
LENGTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 324, Application US/09893737 Patent No. US20020110855A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 329
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.69
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.78
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
OTHER INFORMATION: SWISSPROT HIT: Q04855, EVALUE 2.10e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                        186 KYTAPQPE 193
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TYPE: PRT
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                                                                                                                                                                                                                                                           7 RYTAPQPQ 14
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Evans, Cheryl
     Collins_Racie, Lisa A.
                                                                                                                                                                                                                                                                                             Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                       Score 39; DB 10; Length 295; Pred. No. 17;
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CURRENT APPLICATION NUMBER: US/09/780,016
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 428
TYPE: PRT
RESULT 5
US-09-780-016-18
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                                                                                                                                                                                         ; ORGANISM: homo sapiens US-09-780-016-22
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US-09-780-016-22
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                                                                                                                               Matches
                                                                                                                                               Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020004591A1e1 Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0132-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Donoho, Gregory
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
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PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
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                                                            270 VNGRFTAPQAE 280
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                                                                                           4 IEGRYTAPQPQ 14
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                                                                                                                                         Local Similarity
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US20020004591A1
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                                                                                                                          Conservative
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Spaulding, Vikki
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Treacy, Maurice
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75.08;

 Mismatches

                                                                                                                                Score 39; DB 10; Length 428; Pred. No. 26;
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Pred. No. 26;
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; Sequence 18, Application US/09780016
; Patent No. US20020004591A1
; GENERAL INFORMATION:

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ORGANISM: homo sapiens US-09-780-016-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 26, Application US/09780016; Patent No. US20020004591A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 18
LENGTH: 453
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TITLE OF INVENTION: NO. US20020004591A1el Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0132-USA CURRENT APPLICATION NUMBER: US/09/780,016 CURRENT FILING DATE: 2001-02-09 PRIOR APPLICATION NUMBER: US 60/181,294 PRIOR APPLICATION NUMBER: US 60/181,294 PRIOR FILING DATE: 2000-02-11
                                 US-09-780-016-2
; Sequence 2, Application US/09780016
; Patent No. US2002004591A1
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                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alex
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: No. US20020004591A1el Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0.32-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/780,016
CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/181,294 PRIOR FILING DATE: 2000-02-11 NUMBER OF SEQ ID NOS: 27
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APPLICANT: Donoho, Gregory
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                                                                                                                                                                                                                                                                                                                                              LENGTH:
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les 6; Conserv
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                                                                                                                                              326 VNGRFTAPQAE 336
                                                                                                                                                                                                                                    Local Similarity
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Turner, C. Alexander Jr.
Friedrich, Glenn
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pred. No. 28;
3; Mismatches
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; ORGANISM: homo sapiens US-09-780-016-2
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Best Local Similarity
Graphes 6; Conserv
                                                                                                                                                                                                                                                                                                           ORGANISM: homo sapiens US-09-780-016-24
                               Sequence 20, Application US/09780016
Patent No. US20020004591A1
GENERAL INFORMATION:
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APPLICANT: Sands, Arthur T.
US2020004591A1el Human Proteases and TITLE OF INVENTION: No. US2020004591A1el Human Proteases art TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0132-USA
CURRENT APPLICATION NUMBER: US/09/780,016
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ. ID NOS: 27
NUMBER OF SEQ. ID NOS: 27
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APPLICANT:
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APPLICANT:
                                                                                       US-09-780-016-20
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SEQ ID NO 24
LENGTH: 509
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APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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                                                                                                                                                                                                                                                                    Query Match
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CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020004591A1el Human Proteases and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0.32-USA
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APPLICANT: Donoho, Greapplicant: Scoville,
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Turner, C. Alexander Jr.
Friedrich, Glenn
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                       Gregory
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US-09-864-761-39451
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; ORGANISM: homo sapiens
US-09-780-016-20
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SOFTWARE: Fasc
SEQ ID NO 20
TENGTH: 532
                                                     PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                        PRIOR FILING DATE: 2001-01-30
                                                                                                                                                         PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
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CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,294
PRIOR FILING DATE: 2000-02-11
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020004591A1e1 Human Proteases and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0132-USA
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APPLICANT:
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FILING DATE: 2001-01-30
                 APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
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                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00669 FILING DATE: 2001-01-30
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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; GENERAL INFORMATION
                   / Sequence 2, Application US/09794591
/ Patent No. US20010018198A1
                                                                   RESULT 12
US-09-794-591-2
                                                                                                                                                                  B
                                                                                                                                                                                                                          Query Match
Best Local Similarity
""takes 6; Conserva
                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapien US-09-989-920-184
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1; SEQ ID NO 184
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FEATURE:

FEATURE:

OTHER INFORMATION: MAP TO ACO06075.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BOULD MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BOULD MARROW SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BOULD MARROW SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BOULD MARROW SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BOULD MARROW SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
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US-09-989-920-184
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 101
TYPE: PRT
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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mes 7; Conserv
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75.0%;
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53.8%;

    Mismatches

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Pred. No. 18;
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                                                                                                                                                                                                                                                                                  DB 9; Length 101;
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Query Match
Best Local Similarity
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; ORGANISM: Homo sapiens
US-09-794-591-2
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US-09-995-225-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09995225
Publication No. US20020193584A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                             SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chen, I
APPLICANT: Chu, I
APPLICANT: Dang,
APPLICANT: LOWIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins, TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins, TITLE OF INVENTION. Products Related Thereto and Methods of Using Same FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/794,591
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/145,391
PRIOR FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/995,225
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: PCT/US99/23938
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                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/309,208 PRIOR FILING DATE: 2001-07-31
                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/290,917 PRIOR FILING DATE: 2001-05-14
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/282,358 PRIOR FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: 60/282,356 PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: 60/253,404
PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Endogenous And No. US20020193584A1-Endogenous Versions TITLE OF INVENTION: Receptors
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                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/282,032
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/255,366 PRIOR FILING DATE: 2000-12-12
                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/270,266
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/282,365 PRIOR FILING DATE: 2001-04-06
OTHER INFORMATION: No. US20020193584Alel Sequence
                       FEATURE:
                                          ORGANISM: Artificial Sequence
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                                                                                      LENGTH:
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Lowitz, Kevin P.
Pride, Cameron
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                                                                                                                                  version 3.1
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53.8%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5433
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US-09-782-906-2
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
FULE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                              APPLICANT: Delagrave, Simon
                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09782906 Patent No. US20010051369A1
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APPLICANT:
APPLICANT:
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                                                                                                    APPLICANT: Bylina, Edward J.
APPLICANT: Coleman, William J.
TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic TITLE OF INVENTION: Using Same
FILE REFERENCE: HER-0040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                               CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: 60/185,001
PRIOR FILING DATE: 2000-02-25
                                                                                                                                                                                                                                 APPLICANT:
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0
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TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCHIAI, KEIKO
                                                                                                                                                                                          Murphy, Dennis J.
Maffia III, Anthony M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIZOGUCHI, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANDO, SEIKO
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Pred. No.
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Pred. No. 72;
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79;
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                                                                                                                                             Acid Encoding Same,
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OM protein - protein search, using sw model
January 13, 2003, 09:53:20 ; Search time 12.9231 Seconds (without alignments) 104.146 Million cell updates/sec
                                                                                                                                                GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                             Compugen Ltd.
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Title: Sequence: Perfect score: BLOSUM62 1 QASIEGRYTAPQPQ 14

Searched: Scoring table: 283224 seqs, 96134422 residues Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries

PIR\_73:\* pir2:\* pir3:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

26 27 28 29	24	22	20 21	18 19	17	15	14	13	12	10	. 9	80	7	<b>Б</b> (	л	<b>&gt;</b> (	. K	, 1-1		Result No.
37 5 37 5 37 5	37 5 37 5	37 5 37 5	37 5			38 52	38 52	38 52	38 5	53	лU	· u		ر د	40 54	UT (	40 57	45 51		Score Match
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623 624 625 626 626 768 768 798 1116 1116 1116 1114 4385 5385
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T06794 T00044 F84706 F84706 1504895 1704895 1704881 JC2200 D97695 D97695 1730340 T27684 T29042 T29042 T313142 T313142 T313142
vacuolar sorting r probable vacuolar vacuolar sorting r p-selectin - rat p-selectin precurs homeotic protein p alpha-mannosidase cobn protein homol cobalamin biosynth dsRNA adenosine de hypothetical prote hypothetical prote hypothetical prote protein-tyrosine k 2'.5' RNA ligase (
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# ALIGNMENTS

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RESULT 1
A59232
                                                                                                                                                                                                                                                                                                                                                ABA-responsive protein - barley
C:Species: Hordeum vulgare (barley)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                     A; Reference number: A59232
A; Accession: A59232
                                                                                                                                                                                                                                                                                           R;Liu, J.H.; Luo, M.; Mohapatra, S.S. submitted to GenBank, September 1997
                                                                                                                                                                                                                                                                                                             C;Accession: A59232
R;Liu, J.H.; Luo, M.
                                                                                                                                          A;Cross-references: GB:AF026538; NID:g4103634; PIDN:AAD09343.1; PID:g4103635
A;Experimental source: dev stage embryo
C;Superfamily: barley ABA-responsive protein
                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-326 <LIU>
                                                                                                                                                                                                                                 A; Status: not compared with conceptual translation
밁
                                                                         Matches
   76 LEGKYAAPQP 85
                                                                       Local Similarity es 7; Conserve
                                     4 IEGRYTAPQP 13
                                                                           Conservative
                                                                                                   61.6%;
70.0%;
                                                                                   2; Mismatches
                                                                                                   Score 45; DB 2; Length 326; pred. No. 2.3;
                                                                                                 Gaps
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R;Richardson, M.P.; Braybrook, C.; Tham, M.; Moore, G.E.; Stanier, P. Gene 206, 145-150, 198
A;Title: Molecular cloning and characterization of a highly conserved human 67-kDa la A;Reference number: JC6530; MUID:98121324; PMID:9461426
A;Accession: JC6530 C;Species: Homo sapiens (man) C;Date: 28-Aug-1998 #sequence\_revision 28-Aug-1998 #text\_change 28-Aug-1998 laminin receptor processed pseudogene LAMRL5 - human A; Status: conceptual translation of pseudogene

A; Molecule type:

C;Comment: No evidence could be found that this intronless gene sequence is expressed C;Genetics: A; Residues: 1-295 <RIC> A; Experimental source: brain

C; Keywords: brain; glycoprotein; laminin binding; pseudogene; receptor A; Map position: Xq21.3 A; Introns: #status absent A; Gene: LAMRL5 Best Local Similarity Matches 7; Conserv Query Match 58.9%; Score 43; DB 4; Length 295; 63.6%; Pred. No. 4.7; 3; Mismatches 1; Indels

Conservative

4 IEGRYTAPQPQ 14

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heterocyst glycolipid synthase [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C;Accession: AH2011
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                                                                                                                                                                              RESULT 5
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A; Accession: B75388
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE001994; GB:AE000513; NID:g6459259; PIDN:AAF11071.1; PID:g645920
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-224 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-424 <KAN>
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene: DR1504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Synechocystis sp.
4; Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein - Synechocystis sp. (strain PCC 6803)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda Res. 3, 109-136, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dehydrogenase I, C subunit - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                        80 RYTAPRPQ 87
                                                                                                                                                                                                                                                                                     7 RYTAPQPQ 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 ASIEGRYTAPQP 13
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                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                               56.2%;
87.5%;
                                                                                                                                                                                                                                                                                                                                             Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                        0;
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              RESULT 7
S42471
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C)Keywords: alternative splicing; RNA binding; single-stranded DNA binding F;1-362/Product: single-stranded nucleic acid-binding protein CBP, long form #status F;1-193,225-362/Product: single-stranded nucleic acid-binding protein CBP, short form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 16-51;100-135;287-322 <HAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: CBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: S41652; MUID:93376518; PMID:8367306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 21, 3894, 1993
A;Title: Isolation of a murine gene encoding a nucleic acid-binding protein with homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 12-39;172-193;225-229;306-322 <GOW>
R; Hahm, K; Kim, G; Turck; C; Smale, S:T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X75947; NID:g495127; PIDN:CAA53546.1; PID:g495128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-193,225-300, 'R',302-362 <GOL>
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R;Goller, M.; Funke, B.; Gehe-Becker, C.; Kroeger, B.; Lottspeich, F.; Horak, I.
Nucleic Acids Res. 22, 1885-1889, 1194
A.Title, M.Title, M.Titl
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N.Alternate names: hnRNP protein X
C.Species: Mus musculus (house mouse)
C.Date: 17-ul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Nov-1999
C.Accession: S78515; S45261; S78514; S41652; I48281
R.Hahm, K.B.; Kim, G.; Turch, C.; Smale, S.T.
submitted to the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Murine protein which binds preferentially to oligo-C-rich single-stranded nu
A;Reference number: I48281; MUID:94268912; PMID:8208614
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A; Residues: 1-362 <HAH>
                                                                                                                                                                                                 Matches
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A.Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Recession: AH2011
A;Accession: AH2011
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227 TIQGQYAIPQP 237
                                                                                         3 SIEGRYTAPQP 13
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                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                 Score 39; DB 2; Length 362; Pred. No. 31;
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fasciclin III precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Feb-1990 #sequence_revision 21-Feb-1990 #text_change 24-Sep-1998
C;Accession: A33378
R;Snow, P.M.; Bieber, A.J.; Goodman, C.S.
Cell 59, 313-223, 1989
A;Title: Fasciclin III: a novel homophilic adhesion molecule in Drosophila.
A;Reference number: A33378; MUID:90030406; PMID:2509076
A;Accession: A33378
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A33378
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Eur. J. Biochem. 230, 447-453, 1995
A;Title: Characterisation of two major cellular poly(rC)-binding human proteins, each cd
A;Reference number: S65678; MUID:95331278; PMID:7607214
A;Accession: S65679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1999
A;Reference number: Z21551
A;Accession: T35923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable tRNA synthetase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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                                                   A;Cross-references: GB:M27813; NID:g157423; PID:g157424 C;Genetics:
                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-508 <SNO>
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C; Superfamily: methionine-tRNA ligase
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A; Residues: 1-506 <SEE>
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A;Gene: FlyBase:Fas3
A;Cross-references: FlyBase:FBgn0000636
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les 6; Conserv
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A.Authors: Hunter, J.I.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Kim, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.; Reference number: A86141; MUID:21016719; PMID:11130712

A.; Scatus: Praiferies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein F17F8.23 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein KIAA0434 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 23-Mar-2001
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                                                                                                                                                                                                               C; Genetics:
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A;Cross-references: EMBL:AB007894; NID:g2662148; PIDN:BAA23707.1; PID:g2662149
A;Experimental source: brain; clone HH2165
                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z14082
A; Accession: T00062
                                                                                                                                                                                                                                                                                                                                                                                                 R;Ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, submitted to the EMBL Data Library, October 1997
A;Description: Prediction of the coding sequences of unidentified human genes. VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T00062
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A; Residues: 1-649 <S'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
                                                                                                               Query Match
Best Local
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                                            1 QASIEGRYTAPQPQ 14
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                                                                                           Similarity 7; Conserv
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                                                                                                               53.4%;
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60.0%;
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                                                                                         Score 39; DB 2; wo Pred. No. 1.5e+02; wismatches 5;
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Pred. No.
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Pred. No. 45;
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virulence-associated protein E [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C;Accession: AC3464
                                                                         R;Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; .; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, I Proc. Natl. Acad. Sci. U.S. A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella
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T24965
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A;Gene:
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C81322
                                     A;Reference number: AD3252; PMID:11756688 A;Accession: AC3464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position:
A; Introns: 247/3
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A; Residues: 1-271 <WIL>
A; Cross-references: EMBL: Z68119; PIDN: CAA92195.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, A; Reference number: Z19962 A; Accession: T24965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T18D3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24965
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C;Date: 31-Mar-2000 #sequence_revision
C;Accession: C81322
A;Status: preliminary A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source:
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-75 < PAR>
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nes 7; Conserv
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70.0%;
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46.2%;
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Pred. No.
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Pred. No. 8
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35;
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3.6;
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Search completed: January 13, Job time: 14.9231 secs

2003, 09:57:11

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A;Residues: 1-293 <KUR>
A;Cross-references: GB.AE008917; i
A;Experimental source: strain 16M
C;GenetLcs:
A;Gene: BMEI1697
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                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: H84520
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AC004705; NID:g3252804; PID:g3252813
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T02602; H84520 F. R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: vacuolar sorting receptor protein homolog F26C24.12 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: A+Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02602; H84520
                                                                                                                                                                       A; Map position:
A; Introns: 102/
                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-628 <STO>
                                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z14680
A; Accession: T02602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: I
C; Superfamily: Sphingomonas aromaticivorans
                                                                                                                                                                                                                 A; Gene: F26C24.12; At2g14740
                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                            A; Cross-references: GB:AE002093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-628 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                       Query Match
Best Local
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                                        EGRYTAPQPQ 14
                                                                                                                                                                         102/1; 333/1; 362/3;
                                                                                   Similarity 6; Conserv
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                                                                                   Conservative
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267
                                                                                                       52.1%;
60.0%;
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                                                                                                       Score 38; Pred. No.
                                                                                                                                                                                                                                                            NID: g3252813;
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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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73
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Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_unclassified:*
sp_unclassified:*
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5 Q9KZD6
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                                                              O9ztw0 hordeum vul
O9ztw0 hordeum vul
O9vzr0 drosophila
O95sv2 drosophila
O95sv2 streptomyce
O9xd6 streptomyce
O9yd99 synechocyst
O94099 oryza sativ
O91099 oryza sativ
O91089 deinococcus
O9ru88 deinococcus
O9ru88 drosophila
O95re3 drosophila
O95re3 drosophila
                                                                                                                                                                           Description
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Q9RU88 09ГД99

Q95YM8 Q95RE3 Q9VIT1 Q9A0E7 Q8YWG7 Q29049 Q9VPZ0 Q9UH34

Ogade7 streptococc Ogywg7 anabaena sp Ogywg7 anabaena sp Ogydy9 sus scrofa Ogypz0 drosophila Ogynad homo sapien

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RESULT 1
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Best Local S
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooldeae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pordeum.
Triticeae; Hordeum.
NCBI_TaxID-4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9ZTW0;

O1-MAY-1999 (TIEMBLIE1 10, Last sequence update)

O1-MAY-1999 (TIEMBLIE1 21, Last annotation update)

O1-JUN-2002 (TIEMBLIE1 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ZTW0
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Cheng K.-J., Mohapatra S.S., Hill R.D.; SEQUENCE FROM N.A. Cheng K.-J., Mohapatra S.S., Hill R.D.; Liu J.-H., Luo M., Cheng K.-J., Mohapatra S.S., Hill R.D.; that is a state of the sequence of a novel barley gene that is a light of the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.5
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O9VZR0:
01-MAY-2000 (TIEMBLIEL. 13, CIESTED)
01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
                                                             Q9VZR0
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les 7; Conserv
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0 Q9ETQ3
Q9AMR5
6 Q9PNC6
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1 088737
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Q9P8R1
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                                                                                                                                                                                                                                                     Score 45; DB 10; Length 326; pred. No. 5.9; 1; Indels 2; Mismatches
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Q91008 streptomyce
Q9w702 xenopus lae
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Oppno6 campylobact
Oppno6 raizobium 1
Oppno4 rhizobium 1
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09upa5 homo sapien
09upa5 homo sapien
09ftq3 oryza sativ
09ftq3 bradyrhizob
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Q9zbh7 streptomyce
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09fyh7 arabidopsis
026257 dictyosteli
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o80979 arabidopsis
o80979 arabidopsis
p83027 arabidopsis
p84027 arabidopsis
o8teel homo sapien
o88737 mus musculu
o88737 deinococcus
o987214 deinococcus
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Q9p8r1 sclerotinia
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RX MEDINE-20156006 PubMed-10731132;
RA Adams M.D. Celiker S.E. Holt R.A. Evans C.A. Gocayne J.D. RA Adams M.D. Celiker S.E. Holt R.A. Evans C.A. Gocayne J.D. RA Adams M.D. Celiker S.E. Lip M. Hoskins R.A. Galle R.F. RA Adams M.D. Celiker S.E. Richards S. Rashburner M. Henderson S.M. RA Sutton G.G. Wortman J.R. Yandell M.D. Zhang Q. Chen L.X. Rash Man K.H. Doyle C. Baxter E.G. Helt G. Nelson C.R. Millos G.L.G. Ballew R.M. Sutton G.G. Mortman J.R. Yandell M.D. Holter S.M. Rash Man K.H. Doyle C. Baxter E.G. Helt G. Nelson C.R. Millos G.L.G. Beleson K.Y. Basu A. Baxendale J. Radrews Fennkoch C. B. Baldwin D. Ballew R.M. Sallew R. M. Basu A. Baxendale J. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Basus A. Baxendale J. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Benns P.V. Berman B. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Benns P.V. Berman B. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Benns P.V. Berman B. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Benns P.V. Berman B. Baytaktaroglu L. B. Baldwin D. Beleson K.Y. Benns P.V. Berman B. Baytaktaroglu L. B. Davies P. Ra Cherry J.M. Cawley S. Dahlker H. Gadleu E. Centevtlier P. Rocker M. Cawley S. Dahlker H. Gadleu E. Centevtlier P. Rocker M. Golds R. B. Delcher A. Deng J. P. Bhandari D. Belandra I. B. Davies P. Berman P. B. Davies P. Ra Polate N. Gabrielian A.E. Garg N.S. Gelbart W.A. Classer K. Ra Hortis N. Gabrielian A.E. Garg N.S. Gelbart W.A. Classer K. Ra Hortis N. Gabrielian A.E. Garg N.S. Gelbart W.A. Classer K. Ra Hortis N. L. Harvey D. Helman T.J. Hernandez J. Harris M. Ra Lasko P. Lei Y. Levits A.A. Lid, Li S. Kulp D. Lai Z. K. Ra Lasko P. Lei Y. Levits A.A. Lid, Li S. Kulp D. Lai Z. K. Ra Lasko P. Lei Y. Levits A.A. Nixon K. Nusskern D. R. Paclab J. M. Shull R. Ra Man J. P. Harris S. M. Melbarson D. R. Nelson J. R. Murphy L. Resen M.G. Ra Globs R.A. Woota R. Woota R. D. Woota R. R. Woota R. R. Woota R. W
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Drosophila melanogaster (Fruit fly).
                                                                                                                Q95SV2
Q95SV2;
01-DEC-2001
01-DEC-2001
                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                               93 IKGRHVAPEPQ 103
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Mrai mavin-7777.
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7; Conserv
                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                     58.9%; Score 43; 63.6%; Pred. No.
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Q59995;
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Q95SV2 RESULT 3

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                           451 SIRGLFTAPQP 461
                                                                                                                                                                                                                                                                                "Complete genome sequence of the model actinomycete Streptomyces Nature 417:141-147(2002).
EMBL; AL53870; CAB89014.1; ...
                                                                                                                                                                                                                                                                                                                                                  Bentley S. D. Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                        3 SIEGRYTAPOP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=A3(2) / M145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KZD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9KZD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Champe M., Brokstein P., Hong L., Agbayani A., Carlson J., Geonzalez M., Glarin H., Li P., Liao G., Miranda A., Garlson J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Lewis S.E., Rubin G.M., Celniker S., Phouanenavong S., Wan K., EMBL, AV06/471; AAL25510.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 IKGRHVAPEPQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 IEGRYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                          Similarity
                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                   1) protein.
525 AA; 57338 MW; 4A7BE97C8CAFBB24 CRC64;
                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0035436; CG12016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                 58.98;
72.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.98;
63.68;
                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                           Score 43; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               780E1FC22C297DF2 CRC64;
                                                                                                                                                                                                                           DB 16; Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 5; Length 323;
                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                               ,
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                                                                                                                                                                                       0,
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                methyltransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiura M., Tabata S.;

Sequence analysis of the genome of the unicellular cyanobacterium sequence analysis of the genome of the unicellular cyanobacterium sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb synechocystis sp. strain PCC6803. I. Sequence featu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-PCC 6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96127529; PubMed=8590279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain pCC8803. II. Sequence determination of the synechocystis sp. strain pCC8803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Hirosawa M., Sugiura M., Nakazaki N., Naruo K., Okumura S., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.

-i- SIMILARITY: TO C-5 CYTOSINE-SPECIFIC DNA METHYLASE FAMILY.

EMBL; D64000; BAA10211.1; -
HSSP; P20589; 1DC7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001525; C5_DNA_meth.
Interpro; IPR001525; C5_DNA_methylase; 1.
Pfam; PF00145; DNA_methylase; 1.
PRINTS; PR00105; C5METTRFRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGKER WAS, AND TO THE TOTAL TO THE TOTAL THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methyltransferase; Restriction system; Transferase; C
SEQUENCE 424 AA; 47352 MW; D0428C8FCCC230 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JNN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Core eudicots; Rosid spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q949Y3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
                                                                                                                                                                                                                                                                                                                                                                               Putative acid phosphatase.
Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,
                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA CYTOSINE = S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ASIEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASDKGAYTAPRP 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGR00675; dcm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 424; 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                               core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M., Panna J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., RA Kamiya A., Satou M., Seki M., Nguyen M., Palm C.J., RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K., RA Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki R. RA Sakurai T., Ecker J.R., Theologis A.;
RA Davis R. W., Ecker J.R., Theologis A.;
RA Davis R. W., Ecker J.R., Theologis A.;
RA Davis R. W., Ecker J.R., Theologis A.;
Submitted (NAR-2002) to the EMBL/GenBank/DDBJ databases.
RI CATALYTIC ACTIVITY: AN ORTHOPHOSPHORIC MONOESTER + H(2)0 = AN PROBLEM CONTROL ALCOHOL + PHOSPHATE.

C. ALCOHOL + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Garrinci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length CDNA of gene T5E15 10,AT5934850.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003961; FN III.
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T_phosphtse.
InterPro; IPR004844; S/T_phosphtse.
Pfam; PF00149; Metallophos; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY050812; AAK92747.1; -. EMBL; AY091415; AAM14354.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LD99;
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LD99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            391 QEGLAGRFTEPQP 403
                                                                                                                                                                                                                                                                                           STRAIN=CV. NIPPONBARE: Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto DNA, chromosome 1,
"Oryza Sativa nipponbare(GA3) genomic DNA, chromosome 1,
"Oryza Sativa nipponbare(GA3)
               "OTYZA SALIVA Nipponbare(GAA) genomic DNA, chromosome 1, PAC clone:p0511C01", submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (MAY-2000) BAA96555.1; EMBL, AP002400; BAA96555.1; Interpro; IPR003662; Sub_transporter_UNKNOWN_1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
                                                                                                                                                                                                                                               submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QASIEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iron; Zinc
475 AA; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                               NIPPONBARE;
                                                                                                                                                                                             NIPPONBARE;
             590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pred. No. 32;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7C73A161EE16327E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 475;
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RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Takeuchi H., Kage E., Sawata M., Kamikouchi A., Ohashi K., Ohara M.,
Pujiyuki T., Kunieda T., Sekimizu K., Natori S., Kubo T.,
                                                                    Apis mellifera (Honeybee).
Apis mellifera (Honeybee).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Ac
Apoidea; Apidae; Apis.
                                                                                                                                                      Q95YM8;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9RU88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                       8WX560
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                             Prodom; PD001581; Complex1_30K; 1. PROSITE; PS00542; COMPLEX1_30K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001268; Complex1_30K. Pfam; PF00329; complex1_30Kd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MADLINE-20036896; PubMed-10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphille W., Crosby M., Shen M.,
Vamathevan J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the radioresistant bacterium Deinococcus Science 286:1571-1577(1999).
EMBL; AE001994; AAF11071.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                   80 RYTAPRPQ 87
                                                                                                                                                                                                                                                                                                                           7 RYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NADH dehydrogenase I, C subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RU88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       es 8; Conserv
                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           224 AA; 25032 MW; 05CC3BDF11281B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                   Conservative
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87.5%;
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61.5%;
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                                                                                                                                                                                                                                                                                                                                                                        Score 41;
                                                                                                                                                                                                                                                                                                                                             Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                             No.
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                                                                                                                                                                                                                                                                                                                                          0;
                                                                                  Apocrita; Aculeata;
                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                     0,
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В

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CTIVED
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SEQUENCE FROM N.A.
                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                      Drosophila melanogaster (Fruit fly).
                                                                                                     CG10263 protein.
                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                   CG10263
                                                                                                                                                                     Q9VIT1;
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RT
DR
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                                                                                                                                                                                                                                                                                                                             Zinc-finger.
SEQUENCE 302 AA; 32559 MW; 7A54C93AAIFF32BC CRC64;
                                                                                                                                                                                                                                             248 QAHINHRHVAPQP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q95RE3, PRELIMINARY; PRT; 302 AA.
Q95RE3,
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG10263.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                      1 QASIEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                 Local Similarity
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EMBL; AB047034; BAB64310.1; SEQUENCE 1598 AA; 174929 MW; E5475BDD3ACBlEEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       995 GRYTPPQP 1002
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                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                          54.8%; Score 40; 61.5%; Pred. No.
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87.5%;

    Mismatches

                                                                                                                                                                     PRT;

 Mismatches

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Pred. No.
                                                                                                                                                                  452 AA.
                                                                                                                                                                                                                                                                                                              DB 5; Length 302;
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RA Ballew R.M., Basu A., Baxendare J., Baylan Calogur D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shine B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yell-Y., Shen H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
Q9A0E7
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                                                                                                                                                                                                                                   Q9A0E7;
01-JUN-2001
01-JUN-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pieilier B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Abril J.F., Agbayani A., An H.-J., T. Bender R. M., Baldwin D., Abril J.F., Agbayani A., An H.-J., T. Bender R. M., Baldwin D., Baldwin D., Baldwin D., Baldwin D., Baldwin B., Baldwin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0032812; CG10263.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER. EMBL; AE003663; AAF53834.1; -.
                                                                                                                                                                                                                                                                                                                                                                         Q9A0E7
                                                                                      Streptococcus pyogenes.
Bactlus/Clostridium group; Lactobacillales;
                                                                                                                                                                  Hypothetical protein SPy0807. SPY0807.
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                            Streptococcaceae; Streptococcus. NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 QAHINHRHVAPQP 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                   (TremBLrel. 17, Created)
(TremBLrel. 17, Last sequence update)
(TremBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.8%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    736 AA.
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RESULT 14 Q29049

Q29049 Q29049;

PRELIMINARY;

PRT;

135 AA

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RESULT 13
Q8YWG7
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                                                                                            Query Match
Best Local Similarity
7; Conserve
В
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Best Local Similarity
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                                                                                                                                                                                                                                                                                        EMBL; AP003586; BAB78012.1; -.

InterPro; IPR001227; Ac_transferase.

InterPro; IPR000794; Ketoacy1-synt.

InterPro; IPR008094; Ketoacy1-synt.

InterPro; IPR003880; Ppantne_attach.

Pfam; PF00109; Ketoacy1-synt; 1.

Pfam; PF00109; Ketoacy1-synt; 1.

Pfam; PF00510; Pp-binding; 1.

PROSITE; PS00506; B_KETOACYL_SYNTHASE;

PROSITE; PS00606; B_KETOACYL_SYNTHASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an Ml strain of Streptococcus pyogenes.", Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

EMBL; AE006531; AAK33744.1; ".
InterPro; IR000917; Sulfatase.
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01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
MEDLINE=21192684; PubMed=11296296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; pF00884; Sulfatase; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 736 AA; 82914 MW; A3228642886858EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR 2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8YWG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura
Wishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Naharaki W. Okimana M., Matsumoto M., Matsuno A., Muraki A.,
Naharaki W. Okimana M., Matsumoto M., Matsuno A., Muraki A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heterocyst glycolipid synthase.
1154 LEPRYSAPTPO 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=103690;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                 Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 VKGHYAAPDPQ 259
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                                                            4 IEGRYTAPQPQ 14
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                                                                                                                                                                                                                                                                                              00550; pp-binding; 1.
PS50075; ACP_DOMAIN; 1.
PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cyanobacteria; Nostocales; Nostocaceae; Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                              1263 AA;
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.8%;
                                                                                                                                                  54.8%;
63.6%;
                                                                                                                                                                                                                                              137716 MW; FBA1BFA4A08B1430 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
                                                                                                                            Mismatches
                                                                                                                                                     Score 40; DB 16;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.2e+02;
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                                                                                                                                                                                        Length 1263;
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RESULT 15
Q9VPZ0
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                                                                                                                                                                                                                                                                                                                                     Q9VPZO;
01-MAY-2000
01-MAY-2000
01-MAY-2000
CG5139 prote:
CG5139.
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                             STRAIN-BERKELEY;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                               Q9VPZ0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH-domain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99307156; PubMed=10375634;
Davoli R., Zambonelli P., Bigi D., Fontanesi L., Russo V.;
"Analysis of expressed sequence tags of porcine skeletal muscle.";
"Gene 233:181-188(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2002 (TrEMBLEL 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleocapsid; Ribonucleoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50084; KH_TYPE_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00322; KH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davoli R., Fontanesi L., Cepica S., Musilova P., Stratil A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The porcine Poly(rC)-binding protein 2 (PCBP2) gene maps to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=SKELETAL MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heterogeneous nuclear ribonucleoprotein (Fragment).
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14 TIQGQYAIPQP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 AA; 14144 MW; 8789F8CF3D23F2FC CRC64;
                                                                                                                                                                                                                                                                                                                                                             (TIEMBLrel. 13, Created)
(TIEMBLrel. 13, Last sequence update)
(TIEMBLrel. 13, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB
Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            179 AA.
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                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 135;
Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus.
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Search completed: January 13, Job time: 56.1282 secs
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                δõ
                                 Matches
           51
                         Local
                1 QASIEGRYTAPQP 13
           EAEIQGAITAPNP 63
                         Similarity
                      Conservative
                        53.4%;
  2003, 09:59:48
                     2
                        Score 39;
Pred. No.
                     Mismatches
                          DB 5; Length 179;
                     4.
                     Indels
                     0;
                    Gaps
                     0
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Matches

US-09-133-944-6

OTHER INFORMATION: Description of Unknown Organism: minibody OTHER INFORMATION: presentation structure

Query Match Matches

Local Similarity

Conservative

47.9%; 75.0%;

Mismatches Score 35; DB 4; pred. No. 28;

0;

Indels

0

Gaps

0

Length 70;

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43 ASVKGRYT 50

2 ASIEGRYT 9

US-09-208-827-7 RESULT 6

sequence 7, Application US/09208827 patent No. 6391582

GENERAL INFORMATION:

APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252-1/DJB/DAV

CURRENT APPLICATION NUMBER: US/09/208,827
CURRENT FILING DATE: 1998-12-09
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14
EARLIER FILING DATE: 1998-08-14
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

ENGTH

70

TYPE:

ORGANISM: Unknown

US-09-208-827-7

OTHER INFORMATION: Description of Unknown Organism: minibody OTHER INFORMATION: presentation structure

Query Match Matches

Local Similarity es 6; Conserv 2 ASIEGRYT 9

Conservative

Mismatches Score 35; DB 4; pred. No. 28;

0;

Indels

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Gaps

0;

Length 70;

47.9%; 75.0%;

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43 ASVKGRYT 50

RESULT 7
514582-36
5544582-10.
5514582
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE A.
APPLICANT: CAPON, DANIEL J.; LASKY, LAURENCE HYBRID
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID

0;

; IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:

US/08/185,670

APPLICATION NUMBER: US/08/18
FILING DATE: 21-JAN-1994
FRICOR APPLICATION DATA:
APPLICATION UNMBER: 986,931
APPLICATION NUMBER: 9808,122
APPLICATION NUMBER: 808,122
APPLICATION NUMBER: 440,625
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
FILING DATE: 22-NOV-1989

SEQ ID NO 6 LENGTH: 70

ORGANISM: Unknown

TYPE: PRT

EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 39 SOFTWARE: PatentIn Ver. 2.0

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5514582-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: MOONEY, JEFFREY
                                                                                                                                                       US-08-955-713-4
                                                    밁
RESULT 9
US-08-583-562B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 315,015 FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BERGSMA, DERK
APPLICANT: HALSEY, WENDY
TITLE OF INVENTION: CDNA CLONE HEOAD54 THAT ENCODES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                   TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 120
                                                                                                        Matches
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 QCTSEGVWTPPVPQ 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 23,031
REGISTRATION NUMBER: GH
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. BOX 98
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: LBM COMPUTER: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
SOFTWARE: TOWNTON DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 23-OCT-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 19482
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/050,124 FILING DATE: 18-JUN-1997
                                                   356 QGQHTVPQP 364
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TOPOLOGY: lin
                                                                                                    Local Similarity es 5; Conserv
                                                                              5 EGRYTAPQP 13
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                                                                                                                                                                                                               amino acid
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O. BOX 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                              610-407-0701
                                                                                                           Conservative
                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
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                                                                                                                                                                                                  single
                                                                                                                           47.9%;
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                                                                                                                                                                                                                                                                                                                           GH-70087
                                                                                                                              score 35; DB 2;
pred. No. 2.3e+02;
                                                                                                                  3; Mismatches
                                                                                                                                             DB 2; Length 476;
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US-08-779-113-8
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                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08779113
Patent No. 5948891
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/770 ...
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                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                         STREET: 22.
STREET: Chicago
CITY: Chicago
TRATE: Illinois
Thited
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                  APPLICANT: Staunton, Donald E.
APPLICANT: Harris, Edith S.
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1712 YTAPQP 1717
                                                                                                                                            COUNTRY: Ur
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2647 amino acid
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08583562B Patent No. 5922570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams IT: Joseph A.
REGISTRATION NUMBER: 38 659
REFERENCE/DOCKET NUMBER: 27866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 YTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDAL STREET: 230 CTITY: Chicago rllino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                            INFORMATION:
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                                                                                                                                                 _United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2647 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.9%; Score 35; DB 2; Length 2647; 100.0%; Pred. No. 1.5e+03; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27866/33033
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TOPOLOGY:
US-08-591-989-2
                                          Matches
                                                                     Query Match
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                                                                                                                                                                       TELEFAX: (303) 793-34
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION UNMER: 33, 215
REFERENCE/DOCKET NUMBER: NEX
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10707 1071 2323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ROSS S. Rabin, Sumedha Jayasena
APPLICANT: and Larry Gold
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08591989 Patent No. 5795721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-779-113-8
                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
MEDIUM TYPE: Storage
         6 GRYTAPQPQ 14
                                       Local Similarity es 6; Conserv
                                                                                                                       STRANDEDNESS:
                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Greta E. NO. 5948891and
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/:
TELEPHONE: 312-474-6300
                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COME....-
OPERATING SYSTEM: MS-DOS
CONTWARE: WORD PERFECT 6.0
                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/591,989 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UZIP: 80111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1712 YTAPQP 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Swanson & Bratschun, L.L.C. STREET: 8400 East Prentice Avenue, Suite #200
=:= =:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match
Local Similarity 100.0%; Pred. No. 1.5e+03
hes 6; Conservative 0; Mismatches 0.
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TOPOLOGY: not re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                amino acid
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                                  Conservative
                                                                                                        linear
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                                                                                                                    single
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               46.6%; Score 34; DB 1; Lengtn 230, 66.7%; Pred. No. 1.6e+02; Mismatches 1; Indels
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                                                Length 235;
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                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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26 GRFTAGQPR 34

RESULT 12 US-08-591-989-5

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                 Sequence 2, Application US/08690473 Patent No. 5876923 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08591989 Patent No. 5795721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: ROSS S. Rabin, Sumedha Jayasena
APPLICANT: and Larry Gold
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC
TITLE OF INVENTION: ACID LIGANDS OF ICP4
NUMBER OF SEQUENCES: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,989
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BAITY J. SWANSON
REGISTRATION NUMBER: 33,215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            APPLICANT: Leopardi, Rosario
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.40 MB
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: NEX 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   114 GRFTAGQPR 122
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CITY: E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                   COUNTRY: USA
ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                         STATE:
                                                                                                         STREET:
                                                                                                           ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                       6 GRYTAPQPQ 14
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                                                                                        Houston
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                                                                     Texas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8400 East Prentice Avenue, Suite #200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1;
Pred. No. 2.2e+02;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Sequence 2, Application US/08843659
Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Leopardi, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEY
TITLE OF INVENTION: INHIBITORS OF
                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
****hes 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1298
TYPE: PRT
ORGANISM: HERPES VIRUS, TYPE 1
US-09-259-821A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-259-821A-2
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                                                                                                                                                                                       US-08-843-659-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: LEOPAND, BERNARD
APPLICANT: ROIZMAN, BERNARD
APPLICANT: ROIZMAN, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REFERENCE: ARCD:317
CURRENT APPLICATION UNMBER: US/09/259,821A
CURRENT FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09259821A Patent No. 6210926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
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Best Local Similarity
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REPERENCE/DOCKET NUMBER: ARC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/690,473 PRIOR FILING DATE: 1996-07-26 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Highlander, Steven
                   CORRESPONDENCE ADDRESS
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 GRFTAGQPR 289
                                                                                                                                                                                                                                                                281 GRFTAGQPR 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GRYTAPQPQ 14
                                                                                                                                                                                                                                                                                                   6 GRYTAPQPQ 14
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                                                                                                                                                                                                                                                                                                                                          Conservative
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 Arnold, White & Durkee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.6%;
                                                    HERPES SIMPLEX VIRUS US3 AND ICP4 AS INHIBITORS OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                            46.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/690,473
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                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 4;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2;
Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                               Length 1298;
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                                                                                                                                                                                                                                                                                                                                              1; Indels
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CITY: Houston
STATE: Texas
COUNTRY: United States
ZIP: TOTALO
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Decrease #1.0, Version #1.30

PULLANION NUMBER: US/08/843,659
FILING DATE: Concurrently Herewith
CLASSIFICATION NUMBER: US/08/843,659
FILING DATE: Concurrently Herewith
APPLICATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARSB:519
TELECHONE: (512) 418-3000
TELECHONE: (512) 418
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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                       Title:
Perfect score:
                                                  Total number of hits satisfying chosen parameters:
                                                                                     Searched:
                                                                                                                                    Scoring table:
                                                                                                                                                                         Sequence:
Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                           US-09-554-941-11
73
                                                                                                                                                                                                                                              January 13, 2003, 09:53:15; Search time 14 Seconds (without alignments) 41.476 Million cell updates/sec
                                                                                   112892 segs, 41476328 residues
                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            1 QASIEGRYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                               GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

patabase : SwissProt\_40:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match 1	Length DB	1	ID	ipt
	45	57.5	218	μ !	CLP2_STRCO	
<b>ب</b> د	4 C	אן נ אי אי	362	ш	PCB2_MOUSE	O15366 homo sapier
J K	ب م	53.4	365	<b>د</b> سم	PCB2_HUMAN	homo di
٠ (	٠ د د	5 C	423		WDRC_HUMAN	1 2110
n +₽	יני	53.4	423	<u>س</u>	WDRC_MOUSE	09JJa4 mas masomila
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<b>1</b> C	ب م	2	663	1	TRA_BPMU	
ж ·	37	50.7	138	<u> </u>	DIU1_MANSE	001102 mus musculu
9	37	50.7	768	-	LEM3 MOUSE	
10	37	50.7	768	-	LEM3 CHEED	
11	37	50.7	769	<b>ب</b>	LEMS_SABER	
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13	37	50.7	4.00		PURO MYCTU	
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17	36	49.				
18	w	49.				caenorha
19	w	49.				locusta
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21	(1)	49.		ب.		xenopus
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333 425 682 802 811 902 1033 1531 2647 651 1690
CAP1_DICDI L756_CAEEL RHSE_ECOLI XYND_RUMF1 Y104_SYNY3 GCP2_HUMAN CR2_HUMAN CR2_HUMAN FLNA_HUMAN FLNA_HUMAN ABG5_HUMAN ABG5_HUMAN KF1A_HUMAN KF1A_HUMAN
p19198 dictyosteli Q11184 caenorhabdi P24211 escherichia Q53317 ruminococcu p54317 synechocyst Q9bsj2 homo sapien p20023 homo sapien 094916 homo sapien P21333 homo sapien P21333 homo sapien Q12756 homo sapien Q12756 homo sapien Q12756 chromatium

## ALIGNMENTS

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000000000000000000000000000000000000000	Halo or a series
SEQUENCE FROM N.A.  STRAIN=A3(2) / M145;  STRAIN=A3(2) / M145;  STRAIN=A3(2) / M145;  BentLey S.D. Chater K.F., Cerdeno-Tarraga AM., Challis G.L.,  BentLey S.D. Chater K.F., Cerdeno-Tarraga AM., Kieser H.,  Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,  Phomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Huang CH., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,  Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Fased A., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  Rapholood D.A.;  Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  Rapholood D.A.;  Robinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Rapholoowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Rapholoowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Fased A., Woodward J., Barrell B.G., Parkhill J.,  Fased A., Woodward J., Barrell B.G., Parkhill J.,  Rapholoowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  Rapholoowitsch E., Rapholoo	

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PCB2_MOUSE
ID PCB2_MOUSE STANDARD; PRT; 362 AA.
C 061990; 061383; 062042;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-UN-2002 (Rel. 41, Last sequence update)
DE Poly(rC)-binding protein 2 (Alpha-CP2) (Putative GN PCBP2 OR HNRNPX OR CBP.
                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Makeyev A.V., Liebhaber S.A.;
"Identification of two novel mammalian genes establishes a subfamily of KH-domain RNA-binding proteins.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: SINGLE-STRANDED NUCLEIC ACID BINDING PROTEIN THAT BINDS PREFERENTIALLY TO OLIGO DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                        STRAIN=C57BL/6 X CBA;
                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                  Nucleic Acids Res.
                                                                                                                                                                                                                                                      Goller M., Funke B., Gehe-Becker C., Kroeger B., Lottspeich F.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE (ISOFORM 2).
STRAIN-C57BL/6 X 129/01a; TISSUE-Liver;
MEDLINE-94268912; Pubmed-8208614;
                                                                                                                                                                                                                          "Murine protein which binds preferentially to oligo-C-rich single
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                       Hahm K.B., Kim G., Turch C.,
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93376518; PubMed=8367306
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                      Isolation of a murine gene encoding a nucleic acid-binding protein ith homology to hnRNP K.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; Serine protease; Multigene family; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
                     SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00382; CLP_PROTEASE_HIS; 1.
PROSITE; PS00381; CLP_PROTEASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGRFAMs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00574; CLP_protease; 1
PRINTS; PR00127; CLPPROTEASEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF071885; AAC70948.1; -- EMBL; AL442143; CAC09994.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P19245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THEETPIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S14.UPW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RAASQGRYTGPQAE 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QASIEGRYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGR00493; clpP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001907; CLP_protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lTYF.
                                                                                                                                                                                     (ISOFORM 3)
                                                                                                                                                                                                           22:1885-1889(1994).
                                                                                                                                                                                                                                                                                                                             21:3894-3894(1993).
                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.5%; Score 42; D 50.0%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                     Smale S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67082B89EAC49F2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Putative heterogeneous nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                               -I- SUBCELLUIAR LOCATION: LOOSELY BOUND IN THE NUCLEUS. MAY SHUTTLE BETWEEN THE NUCLEUS AND THE CYTOPLASM.
-I- TISSUE SPECIFICITY: DETECTED IN ALL TISSUES EXAMINED.
-I- PTM: PHOSPHORYLATED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED THE STRONGEST POLY(RC)-BINDING ACTIVITY.
                                         -!- SIMILARITY: CONTAINS 3 KH DOMAINS.
                                                                                                                                                                              proteins,
Eur. J. E
                                                                                                                                         -!- FUNCTION: MAJOR CELLULAR POLY(RC)-BINDING PROTEIN. BINDS ALSO
                                                                                                                                                                                      Leffers H., Dejgaard K., Celis J.E.;
"Characterisation of two major cellular poly(rC)-binding human
                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=95331278; PubMed=7607214;
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2).
                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                        Q15366;
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 TIQGQYAIPQP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50084; KH_TYPE_1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
Repeat; Alternative splicing.
BOWAIN 13 75 KH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF236845; AAK14059 1;
EMBL; AF236842; AAK14059 1; JOINED.
EMBL; AF236843; AAK14059 1; JOINED.
EMBL; AF236844; AAK14059 1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00322; KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:108202; Pcbp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 3 KH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 SIEGRYTAPOP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 6; Conserv
                                                                                                                                                                       Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L19661; AAA03705.1; ... X75947; CAA53546.1; ... X97982; CAA66619.1; ...
                                                                                                                                                                    each containing three K-homologous (KH) alochem. 230:447-453(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1KHM
                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38221 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.4%; Score 39; DB 54.5%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM 2).
MISSING (IN ISOFORM 3).
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KH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70C8AF710E3BF3C0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 362;
                                                                                                                                                                                                                                                                                     HOMinidae; Homo
                                                                                                                                                                         domains.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; x78136; CAA55015.1; ...
HSSP; Q07244; 1KHM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phosphorylation; Repeat-
DOMAIN 13 75
DOMAIN 97 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH_TYPE_1; 3.
Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00322; KH; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; Pr00013; KH-domain; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 601210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                     Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakama K., Ishii S., Kawai Y., Saito K., Wamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Ninomiya K., Iwayanagi T., Ninomiya K., Iwayanagi T., Ninomiya C.DNA sequencing project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OGGZI7; O9NYI8; Q96HUO; Q9NY80;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WD-repeat protein 12 (YTM1 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WDRC_HUMAN
                                                                                                                                                                                                                                                                                                                                                                         "Human homolog of Saccharomyces cervisiae YTM1.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 TIQGQYAIPQP 241
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                           Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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                                                                                                                                               TISSUE-Skin
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                              Submitted (AUG-2000)
use by non-profit institution modified and this statement is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SIEGRYTAPQP 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:8648; PCBP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38580 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.4%; Score 39; DB 1; 54.5%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KH 1.
KH 2.
KH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43F035D76FDC2C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
            not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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29
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                                                                                                                                                                                                                                                                                                      RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; WD :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF242546; AAF60355.1; --
EMBL; AK001743; BAA91875.1; --
EMBL; AK022781; BAB14242.1; --
EMBL; AK022782; BAB14243.1; --
EMBL; AK022782; BAB14243.1; --
EMBL; AC0208082; AAH08082.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000018; WD40; 7 SMART; SM00320; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00320; GPROTEINBRPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genew; HGNC:14098; WDR12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC008082; AAH08082.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00678; WD_REPEATS_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                          Q9JJĀ4; Q9JKF5; Q9CST3;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WD-repeat protein 12 (YTM1 homolog).
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                    WDR12
                                                                                  Depetris D., Verthuy C., Jordan B.R., Ferrier P.; "Wdr12, a mouse gene encoding a novel WD-repeat protein with notchless-like amino-terminal domain.";
                                                                                                                   MEDLINE=21686157; pubMed=11827460;
Nal B., Mohr E., Da Silva M.I., Ta
                                                                                                                                                                                                        Mus musculus (Mouse)
         "Mouse homologue of Saccharomyces cervisiae YTM1.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                           TISSUE=Thymus
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=10090;
                                         STRAIN=129/SVJ X C57BL/6J;
                                                       SEQUENCE FROM N.A.
                                                                           Genomics 79:77-86(2002).
                                                                                                                                                                                                                                                                                                                                     88 KYTAPQPE 95
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                            7 RYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50082; WD_REPEATS_2; 5. PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                             423 AA;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymorphism.
137 WD
                                                                                                                                                                                                                                                                                                                                                                                                                                         75
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286
                                                                                                                                                                                                                                                                                                                                                                                                                             47708 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                              53.4%;
75.0%;
                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi;
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E -> G.
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Pred. No. 15;
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                                                                                                                          Tagett R., Navarro C., Carroll P.,
                                                                                                                                                                                                                                                                                           423 AA
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1).
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RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barshi G.,
RA Blake J., Boffelli D., Bojunga N., Carnita M., Wagner L., Washio T.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
RA Lyons P., Marchionni I., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                       EMBL; AY059431; AAL29680.1; --
EMBL; AY059432; AAL29681.1; --
EMBL; AF239765; AAF44683.1; --
EMBL; AB041608; BAA95091.1; --
EMBL; AK007500; BAB25072.1; --
EMBL; AK012022; BAB27979.1; --
                                 CONFLICT
                                              CONFLICT
                                                                 REPEAT
                                                                                           REPEAT
                                                                                                             REPEAT
                                                                                                                         REPEAT
                                                                                                                                          REPEAT
                                                                                                                                                                        PROSITE; PS50082; WD_REPEATS_2; 5.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                           PROSITE; PS00678; WD_REPEATS_1; 2. PROSITE: PS50082; WD_REPEATS_2; 5.
                                                                                                                                                                                                                                     PRINTS; PR00320; GPROTEINBRPT ProDom; PD000018; WD40; 2.
                                                                                                                                                                                                                               SMART; SM00320;
                                                                                                                                                                                                                                                                        InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                EMBL; BC004748; AAH04748.1; MGD; MGI:1927241; Wdr12.
                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Testis, and Pancreas; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "isolation of full-length cDNA clones from mouse brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                         WD repeat.
99
138
187
255
295
340
384
              423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
                                                                                                                                                                                                                             WD40;
                                                                                                                                                                                                                                                                                                                            BAB30336.1;
                                                                                     137
180
226
293
334
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            47346 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               institutions as long as its content is in
                        WD 1
WD 2
WD 3
WD 4
WD 5
WD 6
F - V
-> S (IN REF. 2).
-> A (IN REF. 1).
DF57952520373667 CRC64;
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RA Addams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA George R.A., Israis S.E., Eli P.W., Hoskins R.A., Galle R.F., RA George R.A., Israis S.E., Richards S.A., Mourter M., Henderson S.N., RA George R.A., Israis S.E., Richards S.A., Ashburner M., Henderson S.N., RA George R.A., Israis S.E., Richards S.A., Ashburner M., Henderson S.N., RA George R.A., Israis S.E., Radell M.D., Zhang O., Chen L.X., RA Birandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., RA Breson K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barliew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Barliew R.M., Basu A., Baxter E.G., Helt G., Nelson D., Botchan M.R., Bouck J., Bayraktargulu L., Beasley E.M., Develow B.D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S.C., Dunn P., Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S.C., Dunn P., Ra Hariis N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Harvey D., Helman T.J., Hernandez J.R., Houck J., Jali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Mattel B., McIncosh T.C., McLeed M.P., McPherson D., Ra Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattel B., McIncosh T.C., McLeed M.P., McPherson D.L., RA RA Liu X., Mattel B., McIncosh T.C., McLeed M.P., McPherson D.L., Ra Ra Laiv K., Melson R.A., Nixon K., Nuskern D.R., Melson D.L., Ra Ra Laiv K., Petalon R.A., Nixon K., Nuskern D.R., Melson D.L., Ra Ra Ra Leiu X., Molariy D.B., Murphy L., Murpy D.M., Nelson D.L., Ra Ra Ra Leiu X., Molariy D.B., Murphy L., Murpy D.M., Nelson D.L., Ra Ra Ra Leiu X., Molariy D.B., Murphy L., Murpy D.M., Nelson D.L., Resee M.G., Shen H., Shen H
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-!- FUNCTION: MEDIATES CELL ADHESION IN A CA-INDEPENDENT MANNER. IT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snow P.M., Bieber A.J., Goodman C.S.; "Fasciclin III: a novel homophilic adhesion molecule in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Berkeley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FAS3_DROME STANDARD; PRT; 508 AA. P15278; Q9VJ89; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fasciclin III precursor (FAS III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAS3 OR CG5803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROME
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75.08;
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Pred. No. 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion; Glycoprotein; Repeat; Immunoglobulin or Transmembrane; Signal; Neurogenesis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M27813; AAA28532.1; -.
EMBL; AE003658; AAF53665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0000636; Fas3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A33378; A33378
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
                                                                                                                                                                                               P07636; P06021;
01-APR-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 33, Last seq
                                                                                                                                                                                                                                       TRA_BPMU
                                                                                                                     Mu-like viruses
                                                                                                                                                            A OR
                                                                                                                                                                      Transposase.
                                                 MEDLINE=86067968; PubMed=2999776; Harshey R.M., Getzoff E.D., Baldw
                                                                                                                                          Bacteriophage Mu
                                                                                                                                                                                                                                                                                                     279 QGRTDGRYSAYEPQ 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: EXPRESSED ON DIFFERENT SUBSETS OF AXON BUNDLES
                         repressor.";
                                      "Primary structure of phage mu transposase: homology to mu
                                                                               SEQUENCE FROM N.A.
                                                                                                     NCBI_TaxID=10677;
                                                                                                                                                                                 11-FEB-1996 (Rel. 33, Last sequence update)
(6-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPING NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLAYS A ROLE IN AXON OUTGROWTH, GUIDANCE AND FASCICULATION OF THE
                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                              1 QASIEGRYTAPQPQ 14
                                                                                                                                                                                                                                                                                                                                                        l Similarity
7; Conserve
              Natl. Acad. Sci. U.S.A. 82:7676-7680(1985).
                                                                                                                                 dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                             508 AA;
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               55883 MW;
                                                                                                                                                                                                                                                                                                                                                                          53.4%;
                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
                                                                                                                                                                                                                                                                                                                                                                          Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MSRIVFICLAAILTD -> MEKQAEISGYAMH (IN REF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION
                                                           Baldwin D.L., Miller J.L.,
                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                6E39EA0580697D4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain;
                                                                                                                                                                                                                                               663 AA.
                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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                                                                  Chaconas G.;
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Priess H., Brauer B., Schmidt C., Kamp D.;
"Sequence of the left end of Mu.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (In) Symonds N., Toussaint A., van de Putte P., Howe M.M. (eds.); Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New York (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toussaint A., Faelen M., Desmet L., Allet B.;
"The products of gene A of the related phages Mu and D108 differ in their specificities.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           priess H., Kamp D., Kahmann R., Braeuer B., Delius H.;
"Nucleotide sequence of the immunity region of bacteriophage Mu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-88 FROM N.A. MEDLINE-83012203; PubMed=6214696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gronenborn A.M., Clore G.M.;
"A novel class of winged helix-turn-helix protein: the DNA-binding domain of Mu transposase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clubb R.T., Omichinski J.G., Savilahti H., Mizuuchi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Gen. Genet. 190:70-79(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98070329; PubMed=9405381; Schumacher S., Clubb R.T., Cai M., Mizuuchi K., Clore G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 76-174.
                                                                                                                                        -I- FUNCTION: THIS TRANSPOSASE IS ESSENTIAL FOR INTEGRATION,
-I- FUNCTION: THIS TRANSPOSITION, AND EXCISION OF MU DNA.
-I- MISCELLANEOUS: MU CAN TRANSPOSE ITS DNA INTO MULTIPLE SITES IN
-I- MISCELLANEOUS: MU CAN TRANSPOSE ITS DNA INTO MULTIPLE SITES IN
MANY BACTERIAL GENOMES AND MEDIATE A VARIETY OF DNA
REARRANGEMENTS. TRANSPOSITION REQUIRES BOTH TRANSPOSASE (ENCODED
BY GENE A) AND TRANSPOSITION ENHANCER (ENCODED BY GENE B).
BY GENE A) AND TRANSPOSITION ENHANCER (ENCODED BY GENE B).
-I- MISCELLANEOUS: UNLIKE OTHER TRANSPOSANS MU HAS DISSIMILAR
-I- MISCELLANEOUS: THE LEFT AND RIGHT ENDS. TRANSPOSASE APPARENTLY BINDS
-I- MISCELLANEOUS: THE A GENE IS REGULATED BY THE REPRESSOR
-I- MISCELLANEOUS: THE A GENE IS REGULATED BY THE REPRESSOR COLLY THE FACT SAME SITES
C CAN, AT HIGH CONCENTRATIONS, OCCUPY ALMOST THE EXACT SAME SITES
C CAN, AT HIGH CONCENTRATIONS, OCCUPY ALMOST THE EXACT SAME SITES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phage Mu transposase: modular DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98035037; PubMed=9367742;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBO J. 16:7532-7541(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solution structure of the Mu end DNA-binding ibeta subdomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural motif for DNA transposition and retroviral integration.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice P., Mizuuchi K.; "Structure of the bacteriophage Mu transposase core: a common {\tt "Structure} of the bacteriophage Mu transposase core: a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95354202; PubMed=7628012;
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                          C CAN, AT HIGH CONCENTRATIONS, COURT TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE, AND TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE, AND TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE AND TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE CAN BIND OF THE TRANSPOSASE CAN BIND ON MU ENDS AS THE TRANSPOSASE CAN BIND ON THE TRANSPOSATION ON THE TRAN
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EMBL outstation

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RESULT 8
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"Isolation and identification of a diuretic hormone from the tobacco hormorm, Manduca sexta.";
Proc. Natl. Acad. Sci. U.S.A. 86:2976-2980(1989).
-!- FUNCTION: REGULATION OF FLUID SECRETION.
                                                                                                                                                         MEDLINE-93066387; PubMed-1279702;
Digan M.E., Roberts D.N., Enderlin F.E., Woodworth A.R., Kramer S.J.;
"Characterization of the precursor for Manduca sexta diuretic hormone
                                                                        Kataoka H., Troetschler R.G., Li J.P., Kramer S.J., Carney R.L.,
                                                                                                                    SEQUENCE OF 81-121
                                                                                                                                                                                                                                              Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
Ditrysia; Sphingiodea; Sphingidae; Sphinginae; Manduca.
                                                                                                  TISSUE=Corpora cardiaca;
                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:11074-11078(1992).
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         MANSE
                                                                                                                                                                                                                                                                                                                     Diuretic hormone 1 precursor (DH-1) (Diuretic peptide 1) (DP-1)
                                                                                                                                                                                                                                                                                                                                       01-MAY-1991 (Rel. 18, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                               P21819;
                                                                                                                                                                                                                                                                                                                                                                                                          DIU1_MANSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02914; Mu_transposase; 1.
Transposition; Transposable element; DNA-binding; DNA excision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         409 ALAGAYTGPNPQ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02316; Mu_DNA_bind;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integration;
BIND 35
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03-DEC-97.
03-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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66
408
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15-OCT-95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.1%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75003 MW;
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P -> S (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               138 AA.
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                                                                                                                                                                                                                                                                                                                                           update)
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       TO CARBOHYDRATES ON NEUTROPHLIS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS STALYL-LEWIS X.

1. SUBCELLULAR LOCATION: Type I membrane protein.

AND WEIEBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL AND WEIEBELS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
      <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                            QQ1102;
QQ1102;
QQ1102;
QQ1-APR-1993 (Rel. 25, Created)
QQ1-APR-1993 (Rel. 25, Last sequence update)
QQ1-APR-1993 (Rel. 41, Last annotation update)
QQ1-QQ2 (Rel. 41, Last annotation update)
QQ2-QQ2 (Rel. 41, Last annotation update)
QQ3-QQ2 (QMP-140) (PADGEM)
QQ3-QQ2 (QMP-140) (PADGEM)
QQ3-QQ2 (QMP-140) (PADGEM)
QQ3-QQ2 (QMP-140) (PADGEM)
                                                                                                                                               Blood 80:795-800(1992).
                                                                                                                                                             MEDLINE=2345617; PubMed=1379089;
Sanders W.E. Jr., Wilson R.W., Ballantyne C.M., Beaude
"Molecular cloning and analysis of in vivo expression
                                                                                                                                                                                                                                        Weller A., Isenmann S., Vestweber D.; "Cloning of the mouse endothelial selectins. Expression of both E-and P-selectin is inducible by tumor necrosis factor alpha."; J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92340571; PubMed=1378846;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEM3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L04628; AAB59200.1; -.
INDUCTION: BY TNF-ALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE SAUVAGINE/CORTICOTROPIN-RELEASING FACTOR/UROTENSIN I FAMILY OF PEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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E; PS00511; CRF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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15296 MW;
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58.3%;
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Pfam; PF00008; EGF; 1.
Pfam; PF00084; Sushi; 8.
Pfam; PF00084; SELECTIN.
PROSITE; PR00343; SELECTIN.
SMART; SM00034; CLECT; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00034; EGF; 1.
SMART; SM000181; EGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS000615; CTYPE_LECTIN_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SIMILARITY: BELONGS TO THE SELECTIN/LECAM FAMILY.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS: MOUSE P-LECTIN LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M87861; AAA40008.1; ...
EMBL; M72332; AAA37712.1; ...
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InterPro; IPR000742; EGF-2.
InterPro; IPR001304; Lectin_C.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR.
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                      DISULFID
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C-TYPE LECTIN (SHORT FO
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Best Local Similarity
5; Conser
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SEQUENCE
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01-FEB-1996 (Rel. 33, Last sequence update)
11-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation protein 140) (GMP-140) (PADGEM)
P-selectin precursor (Granule membrane protein 140) (LECAM3).
(CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
-!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THE
TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
INTERACTION: THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
-!- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED: SPLEEN,
-!- INDUCTION: BY ACUTE INFLAMATION (PROBABLE).
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN/LECAM FAMILY.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN: RAT P-LECTIN LACKS THE
-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS; RAT P-LECTIN LACKS THE
-!- SIMILARITY: CONTAINS 8 SUSHI (SCR) DOMAINS; RAT P-LECTIN LACKS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Rattus norvegicus (Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Murinae; Rat
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 ECTVSGRWSAPPP 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning, sequence comparison and in encoding rat P-selectin.";
Gene 145:251-255(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94333817; PubMed=7520013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
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                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics Institute. There are no restrictions on its buropean Bioinformatics institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by the statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                      InterPro; IPR00056; EGF-like.
InterPro; IPR001304; Lectin_C.
InterPro; IPR002396; Selectin.
InterPro; IPR000436; Sushi_SCR_CCP.
                                                                                                                                                 EMBL; L23088; AAA60325.1; -. HSSP; P16109; 1FSB.
PRINTS; PR00343; SELI
SMART; SM00032; CCP;
                                    pfam; pF00059; lectin_c; 1.
pfam; pF00084; sushi; 8.
                                                                                                                                                                                                                                                                                                                                                       HUMAN SUSHI-2 EQUIVALENT.
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PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
ENDOCYTOSIS SIGNAL (PROBABLE).
A -> E (IN REF. 2).
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RESULT
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Best Local
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P98109;
                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                     SHEEP
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SMART; SM00181; EGF; 1.
PROSITE; PS000022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin; Selectin; Signal; Sushi; Repeat; Lipoprotein; Palmitate.
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                                                                                                                                                                                                                                                                                            768 AA;
                                                                                                                                                                                                                                 Conservative
                                                                                              STANDARD;
                                                                                                                                                                                                                                              50.7%;
                                                                                                                                                                                                                                                                                         83517 MW;
                                                                                                                                                                                                                                          Score 37;
Pred. No.
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BY
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N-LINKED
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SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 7.
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                                                                                          769 AA.
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Pfam; PF00059; lectin_c; 1.
Pfam; PF00084; sushi; 8.
PRINTS; PR00343; SELECTIN.
SMART; SM00032; CCP; 8.
SMART; SM00034; CLECT; 1.
SMART; SM000318; EGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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InterPro; IPR001304; I
InterPro; IPR002396; S
InterPro; IPR000436; S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burns S.A., Neufeld E.J., Donady J.J.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
TO CARBOHYDRATES ON NEUTROPHILS AND MONCYTES. MEDIATES THE
LEUKOCYTES. THE LIGAND RECONNIZED IS STALYL-LEWIS X.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: BELONGS TO THE SELECTIN/LECAM FAMILY.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L34270; AAB59261.1; ... HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-selectin precursor (Granule membrane protein 140) (GMP-140) (PADGEM) (CD62P) (Leukocyte-endothelial cell adhesion molecule 3) (LECAM3).
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NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                     sion; Transmembrane; Glycoprotein; Signal; Sushi; Repeat.
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SUSHI 7.
SUSHI 8.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HMPB_DROME
                                                                                                                                                                                                               cribbs D.L., pultz M.A., Johnson D., American of the "Structural complexity and evolutionary conservation of the prosophila homeotic gene proboscipedia."; EMBO J. 11:1437-1449(1992).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homeotic proboscipedia protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 ECTASGRWTAPPP 565
                                                                                                                                                                                                             EMBO
                                                                                                                                                                                                                                                                              MEDLINE=92224882; PubMed=1348688;
                                                              -!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: At least 4 isoforms; 1 (shown here),
and 4; are produced by alternative splicing.
-!- SIMILARITY: BELONGS TO THE ANTP HOMEOBOX FAMILY.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                               FUNCTION: Sequence-specific transcription factor which is part
                                                                                                                                                  specific positional identifies of controls development of mouthparts,
                                                PROBOSCIPEDIA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Similarity
| 6; Conserv
                                                                                                                                                                 developmental regulatory system that provides cells with secific positional identities on the anterior posterior axis.
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ID YP73_CAEEL
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PIR; S20881; S20881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001827; Antennapedia.
Interpro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS00032; ANTENNAPEDIA; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0025; ANTENNAPEDIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q09222;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 486.0 kDa protein B0228.3 in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516 QQALDGEYLSPKP 528
                                                                                                                                                                                                                                                                                                   Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                             STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                              EMBL; U23168; AAC38807.1; ... WormPep; B0228.3; CE01744.
                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                 Leimbach D., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
  Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T02084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW; 8862B89FAE6C1758 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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TEFVPE -> K (IN ISOFORM
MISSING (IN ISOFORM 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 798;
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PURQ_MYCTU
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                                                                                           or send an email to license@isb-sib.ch).
                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
InterPro; IPR002818; Thij
                  InterPro;
                            TIGR; MT0813; -.
TubercuList; Rv0788;
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                                                                                                                                                                                                                                                                                                                                                              STRAIN-CDC 1551 / Oshkosh; Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hirrisby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the "complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98295987; PubMed=9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID-1773;
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P71841;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PURO OR RV0788 OR MT0813 OR MTCY369.32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphoribosylformylglycinamidine synthase
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16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                      Z80226; CAB02378.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 SIEGRYTAPQPQ 14
                                                   AE006971; AAK45055.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 7; Conserv
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         GATase_1.
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58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50B8871B6C45FA23 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I (EC 6.3.5.3) (FGAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4385;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                             "Characterization of a new cobalt-containing nitrile hydratase purified from urea-induced cells of Rhodococcus rhodochrous J1.";

PUNCTION: NHASE CATALYZES THE HYDRATION OF VARIOUS NITRILE COMPOUNDS TO THE CORRESPONDING AMIDES. INDUSTRIAL PRODUCTION OF ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.

ACRYLAMIDE IS NOW BEING DEVELOPED USING SOME OF THESE ENZYMES.

CATALYTIC ACTIVITY: An aliphatic amide = a nitrile + H(2)O.

SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.

INDUCTION: BY COBALT AND UREA OR CYCLOHEXANECARBOXAMIDE.

SYMILARITY: BELONGS TO THE NITRILE HYDRATASE SUBUNIT BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
                                                                                                                                                                                                                                                                                                          Nagasawa T., Takeuchi K., Yamada H.;
                                                                                                                                                                                                                                                                                                                        MEDLINE=91192028; PubMed=2013281;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-28.
                                                                                                                                                                                                                                                                                                                                                                                                              hydratase (H-NHase) induced by its reaction product in Rhodococcus
                                                                                                                                                                                                                                                                                                                                                                                                                         Komeda H., Kobayashi M., Shimizu S.;
"Characterization of the gene cluster of high-molecular-mass nitrile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96210630; PubMed=8633053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1129:23-33(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning, nucleotide sequence and expression in Escherichia coli of
two cobalt-containing nitrile hydratase genes from Rhodococcus
rhodochrous Jl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1991 (Rel. 18, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
High-molecular weight cobalt-confaining nitrile hydratase subunit beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kobayashi M., Nishiyama M., Nagasawa T., Horinouchi S., Beppu T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92096459; PubMed=1840499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 1-28 AND 69-78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodococcus rhodochrous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 4.2.1.84) (H-nitrilase) (H-NHase).
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Purine biosynthesis; Ligase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01965; ThiJ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AA;
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75.0%;
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    Mismatches

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1; 46B37215D1171D4E CRC64;
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Donald ith Vitoplasmic Modulators of Integrin O'Tople, Gerstein, Murray & Borun Sker Drive, 6300 Sears Tower Borun 1.25  1. Sk tible OS/MS-DOS aase #1.0, Version #1.25  1. Sph A. 258  27866/33033	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	APPLICANT: Nefsky, Bradley NUMBER OF INVENTION; Diquitin Ligases, and Uses Related Thereto CORRESPONDENCE ADDRESS: STREET: One Post Office Square COUNTEY, Maton COUNTEY, Maton
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US-08-583-562B-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 8, Application US/08779113 ; Patent No. 5948891
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                В
; Sequence 2, Application US/08956242C ; Patent No. 5986081
                               RESULT /
US-08-956-242-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2647 amino acids
                                                                                                                                                            Matches
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1712 YTAPQP 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         TELEFAX: 312-4/4-0448
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Staunton, Donald E. APPLICANT: Harris, Edith S. TITLE OF INVENTION: Cytoplasmic Modulators of Integrin TITLE OF INVENTION: Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 37
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,474-6300
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 5948891and
REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                  1712 YTAPQP 1717
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                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATEN PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/779,113
                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                 5 YTAPQP 10
                                                                                                                                                                      Local Similarity 100.0%; P
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233 South Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
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                                                                                                                                                                                                                                                                                             2647 amino acids
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                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.4%; Score 35; DB 2; Length 2647; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                  61.4%; Score 35; DB 2; Length 2647; 100.0%; Pred. No. 1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                                                 Gaps
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GENERAL INFORMATION:
APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
APPLICANT: Titus, Polynucleotides Encoding Herg-3
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296.94550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-956-242-2
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                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure (542); LOCATION: (441)...(542); OTHER INFORMATION: Unidentified at time of filing US-09-351-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/351,215
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
EARLIER FILING DATE: 1997-10-22
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09351215 patent No. 6087488 GENERAL INFORMATION:
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                                                                                                            Sequence 4, Application US/08910925
Patent No. 6162601
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                                                                                                                                                   US-08-910-925-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ganetzky, Barry S. APPLICANT: Titus, Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Unidentified at time of filing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure LOCATION: (441)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapien FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                   Query Match 59.6%;
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 626
                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 626
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es 6; Conserv
                                 APPLICANT: Lal, Preeth
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUI
CORRESPONDENCE ADDRESS:
                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ASSYTAPOPO 11
                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                       67 SSHYTFPRPQ 76
                                                                                                                                                                                                                                                      2 ASSYTAPQPQ 11
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                                                                     Lal, Preeti
                                                                                    Bandman, Olga
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                                      HUMAN PININ SPLICE VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                 Score 34; DB 3;
Pred. No. 3.2e+02;
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US-09-314-268-94
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US-09-314-268-94
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                              Matches
                                                             Query Match
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: DOORDAY, JOHN
TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR PAPILLOMA
TITLE OF INVENTION: VIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-910-925-4
                                                                                                                                                  SEQ ID NO 94
                                                                                                                                                                                   FILE REFERENCE: 3789/80902
CURRENT APPLICATION NUMBER: US/09/314,268
CURRENT FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: 09/314,268
EARLIER FILING DATE: 1999-05-18
                                                                                                                                                                                                                                                                                                                             Sequence 94, Application US/09314268
Patent No. 6346377
                                                                                                                                                            NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                             ORGANISM: Human papillomavirus type 54
                                                                                                                         TYPE: PRT
                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GenBan
CLONE: 1684843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                     Local Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                      484 QAQSLPQPQPQ 494
1 QASSYTAPQ 9
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LENGTH: 703 amino acid
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SOFTWARE: FASTSEQ for I
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               match 59.6%;
Local Similarity 63.6%;
es 7; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: Herew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incylc...
STREET: 3174 Porter Drive
                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             703 amino acids
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                                 Score 33; DB
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 3.7e+02;
0; Mismatches 4; Indels
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                 Mismatches
                                           DB 4; Length 35;
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              0;
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SGO ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 209
                                                                                                                                                                                                RESULT 13
US-09-109-100-11
                                                                                                                                          Sequence 11, Application US/09109100C
Patent No. 6291661
GENERAL INFORMATION:
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SEQ ID NO 11
                   APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FL73-L MUTANTS AND METHODS OF USE
FILE REFERENCE: 03260.0028
CURRENT APPLICATION NUMBER: US/09/109,100C
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
COURTMANDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us-09-109-100-9
          SOFTWARE: PatentIn Ver.
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Patent No. 6291661
GENERAL INFORMATION:
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CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 209
TYPE: PRT
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APPLICANT: Graddis, Thomas J.
APPLICANT: McGrew, Jeffrey T.
TITLE OF INVENTION: FLT3-L
FILE REFERENCE: 03260,0028
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                                                                                                                                                                                                                                                               149 EATAPTAPQP 158
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60.0%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                          DB 4;
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RESULT 15

US-09-109-100-13

Sequence 13, Application US/09109100C

Patent No. 6291661

GENERAL INFORMATION:

APPLICANT: Graddis, Thomas J.

APPLICANT: McGrew, Jeffrey T.

APPLICANT: McGrew, Jeffrey T.

ITTLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

FILE REFERENCE: 03260.0028

CURRENT APPLICATION NUMBER: US/09/109,100C

CURRENT FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 13

LENGTH: 209

TYPE: PRT

ORGANISM: Homo sapiens
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US-09-109-100-12

Sequence 12, Application US/09109100C

Patent No. 6291661

GENERAL INFORMATION:

APPLICANT: GCATEM, Jeffrey T.

APPLICANT: MCGIEW, Jeffrey T.

TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE

FILE REFERENCE: 03260.0028

CURRENT FILING DATE: 1998-07-02

NUMBER OF SEQ ID NOS: 20

SOFTMARE: PatentIn Ver. 2.1

SEQ ID NO 12

LENGTH: 209

TYPE: PAT

US-09-109-100-12
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-11
Search completed: January 13, 2003, 09:56:24 Job time: 11.5897 secs
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Best Local (
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Best Local Similarity 60.0%;
Matches 6; Conservative
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149 EATAPTAPQP 158
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                                                                                                                              Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 60.0 nes 6; Conservative
                                                                                               1 QASSYTAPQP 10
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                                                                                                                                 Conservative
                                                                                                                                               57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.9%;
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                                                                                                                                             Score 33; DB 4; Length 209; Pred. No. 1.5e+02;
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Pred. No. 1.5e+02;
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                                                                                                                                 Mismatches
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OM protein - protein search, using sw model

January 13, 2003, 09:54:16;

Run

Title: Perfect score:

US-09-554-941-2 57

1 QASSYTAPQPQ 11 BLOSUM62

scoring table: sequence:

Gapop 10.0 , Gapext 0.5 118974 seqs, 19401057 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

post-processing: Minimum Match 100% Maximum Match 100% Maximum first 45 summaries

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Result No.

Score

Query Match Length DB

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64.9 63.2 63.2 61.4 61.4 59.6 59.6 59.6 57.9

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pred. No. is the number of results predicted by chance to have a pred. No. is the number of the score of the result being printed, score greater than or equal to the score distribution. and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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2: /cgn2_6/ptodata/1/pubpaa/USOG_NEW_PUB.pep:*
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10 US-09-782-906-3
10 US-09-782-906-5
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11 US-09-864-761-33417
10 US-09-864-761-33417
10 US-09-864-761-35691
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10 US-09-788-626-6715
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US-09-904-536-9
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                                                                                   sequence 2, Appli
sequence 3, Appli
sequence 4, Appli
sequence 3, Appli
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sequence 324, App
sequence 160, App
sequence 18, Appli
sequence 18, Appli
sequence 6, Appli
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sequence 947, App
sequence 947, App
sequence 195, Ap
sequence 543, App
sequence 543, Appli
sequence 5, Appli
sequence 1, Appli
sequence 1, Appli
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                                         sequence 11, Appl
sequence 12, Appl
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APPLICANT: Delagrave, Simon
APPLICANT: Mutphy Dennis J.

APPLICANT: Maffia TIT, Anthony M.
APPLICANT: Bylina, Edward J.

APPLICANT: Bylina, Edward J.

APPLICANT: Bylina J.

APPLICANT: Bylina J.

APPLICANT: Some
TITLE OF INVENTION: Using Same
TITLE OF INVENTION USING Same
TITLE OF INVENTION NUMBER: 05010702-14

CURRENT FILING DATE: 2001-02-15

PRIOR APPLICATION NUMBER: 60/185,001

CURRENT FILING DATE: 2000-02-25

PRIOR PRIOR TILING DATE: 2000-02-25

PRIOR PRILING DATE: 2000-02-25

PRIOR PRICH DATE: 2000-
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Patent NO. USZ0010051369Al
PATENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT Dactylium dendroides ORGANISM: Dactylium dendroides US-09-782-906-2
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Best Local S:
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                                                                                         Sequence 3, Application US/09782906; Sequence 3, Application US/09782906; Patent No. US20010051369A1; Patent INFORMATION: Simon GENERAL Delagrave, Simon Applicant: Rittenhouse Pruss, Jennifer L. Applicant: Rittenhouse
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hes 10; Conservative
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5 10 US-09-948-378-1

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5 10 US-09-983-450-1

5 10 US-09-853-450-1

9 US-09-853-270-2

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1 0 US-09-796-692-1764

9 US-09-796-692-1764

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US-09-904-536-10
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100.0%; Pred. No.
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US-09-864-761-42170
US-09-864-761-39451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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sequence 16,
sequence 17,
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APPLICANT: Delagrave, Simon
APPLICANT: Ritechnouse Pruss, Jennifer L.
APPLICANT: Murphy, Dennis J.
APPLICANT: Murphy, Dennis J.
APPLICANT: Murphy, Dennis J.
APPLICANT: Bylina, Edward J.
TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, Villiam J.
TITLE OF INVENTION: Using Same
CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT APPLICATION NUMBER: 2001-02-14
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 639
LENGTH: 639
                                                                                                                                                                                                                                 US-09-782-906-5
                                                                                                                                               Sequence 5, Application US/09782906
Patent No. US20010051369A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: NO. US20010051369Alel Sequence
                                                                                                                                 APPLICANT: Delagrave, Simon
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                                                                                                                                                                                                                                                                                                   147 QASSYTAPQP 156
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CURRENT APLICATION NUMBER: US/09/782,906

PRIOR APPLICATION NUMBER: 05/09/782,906

PRIOR APPLICATION NUMBER: 60/185,001

PRIOR FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.0

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APPLICANT: Coleman, William J.
TITLE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, And Method
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Maffia III, Anthony M.
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100.08; Pre
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CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-02-04
PRIOR PRIOR PRIOR DATE: 2000-05-26
PRIOR PRIOR PRIOR DATE: 2000-05-26
PRIOR PRIOR PRIOR DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PRIOR DATE: 2000-08-03
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2000-08-03
PRIOR PRIOR PRIOR DATE: 2000-08-03
PRIOR PRIOR PRIOR PRIOR NUMBER: US 60/236,359
PRIOR PRIOR PRIOR PRIOR NUMBER: PCT/US01/00666
PRIOR PRI
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APPLICANT: Murphy, Dennis J.
APPLICANT: Murphy, Dennis J.
APPLICANT: Murphy, Dennis J.
APPLICANT: Bylina; Edward J.
APPLICANT: Coleman, Milliam J.
ITILE OF INVENTION: Variant Galactose Oxidase, Nucleic Acid Encoding Same, CURRENT APPLICATION NUMBER: US/09/782,906
CURRENT APPLICATION NUMBER: US/09/782,906
PRIOR APPLICATION NUMBER: 60/185,001
PRIOR APPLICATION NUMBER: 60/185,001
SOFTMARE: PROS ED ID NOS: 8
SEQ ID NO 5
Patentin version 3.0
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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TYPE: PRT
ORGANISM: Artificial
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US20020048763A1
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91.2%; Score 52; DB 10; Length 639; 100.0%; Pred. No. 0.14; 0; Mismatches 0; Indels

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RESULT 4

В

Matches

## Mon Jan 13 10:35:13 2003

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PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-29

PRIOR PRIOR DATE: 2001-01-29

PRIOR FILING DATE: 2001-01-19

PRIOR APPLICATION NUMBER: PCT/USO1/00670

PRIOR APPLIC
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 23
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 23
OTHER INFORMATION: EXPRESSED IN HEAL, SIGNAL = 28
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 28
OTHER INFORMATION: EXPRESSED IN HEALINO, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN HEALINO, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN BOLLT LIVER, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN BOLLT LIVER, SIGNAL = 17
OTHER INFORMATION: EXPRESSED IN BOLLT LIVER, SIGNAL = 29
OTHER INFORMATION: EXPRESSED IN LOW, SIGNAL = 20

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CURRENT PLILING DATE: 2001-06-28
CURRENT PLILING DATE: US 60/215,446
PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 329
NUMBER OF SEQ ID NOS: 329
SOFTWARE: FAST-SEQ for Windows Version 3.0
LENGTH: 295
ENGTH: 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 324, Application US/09893737 sequence 324, Application US/09893737 patent No. US/0020110855Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
US-09-893-737-324
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APPLICANT: Presnell Scott R.
APPLICANT: Presnell Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
TITLE REFERENCE: 000-41
                                                                                                                                                                                                                                                                                                     g
US-09-729-674-160
US-09-729-674-160, Application US/09729674
; Sequence 160, US20010039335A1
; Patent NO. US20010039335A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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72 QATTLTAPQP 81
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conservative
35
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                                                                                                                                                                                                                                                                                                     187 YTAPQPE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity es 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOY, John M.
APPLICANT: Lavallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Evans, Cheryl
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FILE REPERENCE: 1055-64X
FILE REPERENCE: 1055-64X
CURRENT APPLICATION UNBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: 09/539,330
CURRENT FILING DATE: 2000-3-30
PRIOR APPLICATION NUMBER: 09/539,330
DRIOR APPLICATION NUMBER: 09/539,330
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Wright, Daniel F.

APPLICANT: Voytas, Daniel F.

APPLICANT: VENTION; Plant Retroelement

TITLE OF INVENTION; Plant Retroelement

TITLE REFERENCE: P.1065 ISURF Plant Retroelement

PILE REFERENCE: P.1065 ISURF PLANT RETROELEMENT PRIJECATION NUMBER: US/09/965.553

FILE REFERENCE: P.1086-27

CURRENT ILING DATE: 1999-05-28

PRIOR APPLICATION NUMBER: 60/087125

PRIOR APPLICATION NUMBER: 60/087125

PRIOR APPLICATION 1998-05-29

PRIOR APPLICATION NUMBER: 60/087125

PRIOR FILING DATE: 1998-05-29

PRIOR FILING DATE: 1998-05-29

PRIOR FILING DATE: 1998-05-29

PRIOR PRILING DATE: 1998-05-29

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PRIOR FILING DATE: 1998-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
US-09-965-553-8
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Artificial Sequence: plant ORGANISM: Artificial Sequence: plant FEARTURE: OFFICE INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: retroelement sequence: OTHER INFORMATION: Tetroelement Sequence: OTHER 1050RMATION: OTHER 1050RMATIO
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Best Local S
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RESULT 9
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Steininger II, Robert J.
Spaulding, Vikki
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Treacy, Maurice
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Clark, Hilary
                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                 36 EGSSYTSPPP 45
                                                                                                                                                                                     1 QASSYTAPOP 10
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                     score 36;
pred. No.
                                                                                                                                                                                                                                                                                                                            Mismatches
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APPLICANT: Rank, Sharton 6
APPLICANT: Rank, David R
APPLICANT: Rank, David R
APPLICANT: Rank, David R
APPLICANT: Chen, Mensheng
TITLE OF INVENTION: HUMAN GROWNE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR PRICE ACID ACID STATE: 2001-05-23
PRICE APPLICATION NUMBER: US 60/207.456
PRICE FILING DATE: 2000-05-26
PRICE FILING DATE: 2000-05-27
PRICE FILING DATE: 2001-05-20
PRICE FILING DATE: 2001-0
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APPLICANT: Wight, David A.
FILE CANT: Wytas, Daniel F.
FILE OF INVENTION: Plant Retroelements and Methods Related Thereto CURRENT APPLICATION NUMBER: US/09/965,553
FILING DATE: 109-05-28
PRIOR APPLICATION NUMBER: 09/322,478
PRIOR APPLICATION NUMBER: 60/087125
PRIOR APPLICATION NUMBER: 60/087125
SOFTMARE: PATCH APPLICATION NUMBER: 60/087125
SOFTMARE: PATCH SOME: 1998-05-29
SOFTMARE: PATCH SOME: 1998-05-29
SOFTMARE: PATCH SOME: 1998-05-29
SOFTMARE: PATCH SOME: 1998-05-29
SEQ ID NO: 18
LENGTH: 1802
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.00,
6; Conservative
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
US-09-965-553-18
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BALENT NO. US20020112259A1
GENERAL INFORMATION:
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60.0%; Pred. No. 2
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hes 2; Indels
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                                                                            PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR EILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/259162
PRIOR APPLICATION NUMBER: JP 00/280988
IN UMBER OF SEQ ID NOS: 7059
SEQ ID NO 6745
LENGTH: 301
;
US-09-738-626-6745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO AC006391.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 2
OTHER INFORMATION: EXPRESSED IN BOAL MARROW, SIGNAL - 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 2.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 2.2
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 1.6
OTHER INFORMATION: EXPRESSED IN HBLLOO, SIGNAL - 1.6
OTHER INFORMATION: EXPRESSED IN HBLLOO, SIGNAL - 1.6
OTHER INFORMATION: EXPRESSED IN LONG, SIGNAL - 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 1.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 3.5
US-09-864-761-35691 EXPRESSED IN ADULT LIVER, SIGNAL - 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
US-09-738-626-6745
; Sequence 6745, Application US/09738626
; Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/738,626
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PRILING DATE: 2001-01-29
PRIOR PRILING DATE: 2001-01-29
PRIOR PRILING DATE: 2001-01-29
PRIOR PRILING DATE: 2001-01-29
PRIOR STANDAMAN Sequence Listing Engine vers. 1.1
PRIOR SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                     YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                       OZAKI, AKIO
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RESULT 12
US-09-764-864-1515
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US-09-764-864-947
: Sequence 947, Application US/09764864
: Patent No. US20020132753A1
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                                RESULT 14
US-09-764-864-1095
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                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-947
                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 947
LENGTH: 323
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1515
LENGTH: 294
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Sequence 1095, Application US/09764864 Patent No. US20020132753A1
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CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
                                                                                                                                                                             SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 5433
LENGTH: 407
TYPE: PRT
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR TILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PRIOR APPLICATION NUMBER: JP 99/377484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROS
APPLICANT: ANDO, SEIKO
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CURRENT FILING DATE: 2001-01-17
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SENOH, AKIHIRO
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OCHIAI, KEIKO
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	ALIGNMENTS	AAG6358			ABB05144				ABBOULUT	ABBUS130	ABB05137	ABB05136	AAE12968	AAE1296/	AAE12966	AAE12965	AAE12964	AAE12963	AAE12962	AAE12961	AAE12960	AAE12959	AAE12958	AAE12946	AAE12945	AAE12944	AAE12942	33513941	251	Æ	AE12	AE1293	AE1293	
		Amino acid sequenc	۰,		Ф	ወ	Galactose oxidase		CELLINO		Ø	oxidas				Dactylium dendroid	Dactylium dendroid	pactylium dendroid		pactylium dendroid		pactylium dendroid	nactylium dendroid	pactylium dendroid					Dactylium dendroid		-		Dactylium dendroid	

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Galactose oxidase linker used to make proteinase inhibitor fusions.
                                                                                                                                                                                                                                                    AAY22919;
                                                                                                                                                                                                                                                                    AAY22919 standard; peptide; 11 AA.
                                                                                                                                                                                      peptide linker; fusion protein; pathogen resistance; pathogen tolerance;
plant; transgene; proteinase inhibitor; Arabidopsis thaliana;
                                                                                                                                                                                                                                   19-AUG-1999 (first entry)
                                                                                                                                                                             parasitic nematode.
                                                                                                                                           WO9928484-A1.
                                                                                                                                                            Synthetic.
                                                                    (NOVS ) NOVARTIS AG.
                                                                                                         01-DEC-1998;
                                                                                                                           10-JUN-1999.
                                                   Atkinson HJ, McPherson MJ,
                                                                                        03-DEC-1997;
Claim 9; Page 23; 39pp; English.
                                  WPI; 1999-385387/32.
                 proteinase inhibitor fusion proteins
                                                                                          97GB-0025556.
                                                                                                            98WO-EP07792
                                                           Urwin PE;
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RESULT 2
AAE12925
                  The invention relates to variant galactose oxidase (vGO) proteins and their cDNA molecules. Galactose oxidases are useful for oxidising D-galactose side chains of many complex compounds such as guar, major glycolipid of human red cells. GO is useful in paper making processes, generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp biodieaching, the use of GO-Schiff's reagent for early detection and prognosis in human colorectal adenocarcinoma and use of GO-glucan plaque bacteria. GO is useful as a research tool for identification, characterisation and material as a research tool for identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterisation and purification of interacting regulatory proteins
                                                                                                                                                                                                                                                         Example 1; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                 Novel variant galactose oxidase enzyme for oxidizing a compound such as guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAD21273.
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-648219/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HERC ) HERCULES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-FEB-2000; 2000US-185001P.
14-FEB-2001; 2001US-0782906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2001; 2001WO-US05732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dactylium dendroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pulp biobleaching; colorectal adenocarcinoma; dental plaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galactose oxidase; GO; paper making; aldehyde synthesis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dactylium dendroides wild type galactose oxidase (GO) mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE12925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE12925 standard; Protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a peptide linker used in the fusion proteins of the invention. The specification describes a method for improving pathogen resistance or tolerance of a plant. The method fusion protein which comprises two or more protein or domains that are capable of improving pathogen resistance or tolerance when inhibitors are co-delivered, as a fusion, to Arabidopsis thatianis are connected by a peptide linker. The method is used to improve pathogen resistance or tolerance of a plant and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        descendants, especially against parasitic nematode attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QASSYTAPQPQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QASSYTAPQPQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Delagrave S, Murphy DJ, Rittenhouse Pruss J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 57; DB 20;
Pred. No. 0.0018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bylina E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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ΧX
      The invention relates to variant galactose oxidase (vGO) proteins and their cDNA molecules. Galactose oxidases are useful for oxidising D-galactose side chains of many complex compounds such as guar, major glycolipid of human red cells. GO is useful in paper making processes, generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp biobleaching, the use of GO-Schiff's reagent for early detection and prognosis in human colorectal adenocarcinoma and use of GO-glucan plaque bacteria. GO is useful as a research tool for identification, characteristics and main colorectal as a research tool for identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE12926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
characterisation and purification of interacting regulatory
                                                                                                                                                                          Claim 10; Page 45; 65pp; English.
                                                                                                                                                                                                          Novel variant galactose oxidase enzyme for oxidizing a compound such guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                                                                                                                                                                                                                       WPI; 2001-648219/74.
N-PSDB; AAD21274.
                                                                                                                                                                                                                                                                                                                                                    Maffia AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                        Coleman WJ;
                                                                                                                                                                                                                                                                                                                                                                              (HERC ) HERCULES INC
                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-2000; 2000US-185001P.
14-FEB-2001; 2001US-0782906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2001; 2001WO-US05732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 494 /wild type Tyr substituted with His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dactylium dendroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dactylium dendroides galactose oxidase GO8-1 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12926 standard; Protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE12926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidase (GO) mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 QASSYTAPQP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is Dactylium dendroides wild type galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QASSYTAPQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                   Delagrave S, Murphy DJ, Rittenhouse Pruss J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 639 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Wild type Val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Cys substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 639;
                                                                                                                                                                                                                                                                                                                                Bylina E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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The present sequence is Dactylium dendroides galactose oxidase (GO)

밁 20

147 QASSYTAPQP 156

Query Match Best Local S

Local Similarity 1 QASSYTAPQP 10

Sequence variant.

639 AA;

Matches

10;

Conservative

100.0%; 91.2%;

0

Mismatches

Score 52; DB 22; Length 639; pred. No. 0.82;

0 Gaps

RESULT

AAE12927 standard; Protein; 639 AA.

AAE12927;

Dactylium dendroides galactose oxidase GO8-1H3A variant.

(first entry)

Galactose oxidase;

biobleaching; colorectal adenocarcinoma;

GO; paper making; aldehyde synthesis; detection; colorectal adenocarcinoma; dental plaque; variant;

synthetic

Location/Qualifiers

note= "Wild type Gln substituted with Lys"

/note= "Wild type Gly substituted with Ala" Misc-difference 383 /note= "Wild type Cys substituted with Ser" Misc-difference 436

Misc-difference 494

/note= "Wild type val substituted with Ala"

WO200162938-A2.

30-AUG-2001.

Dactylium dendroides. mutant; mutein.

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The invention relates to variant galactose oxidase (vGO) proteins and their cDNA molecules. Galactose oxidases are useful for oxidising their cDNA molecules. Go f many complex compounds such as guar, major D-galactose side chains of many complex compounds such as guar processes, glycolipid of human red cells. GO is useful in paper making processes, pulp generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp generation of the use of GO-Schiff's reagent for early detection and biobleaching, the use of GO-Schiff's reagent for early detection
                                                                                                                                                   Novel variant galactose oxidase enzyme for oxidizing a compound such as guar which is useful in paper making, for enzymatic synthesis of guar which is useful in paper making, the substituted amino alidenydes and pulp biobleaching, has at least one substituted amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                             Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prognosis in human colorectal adenocarcinoma and use of GO-glucan prognosis in human colorectal adenocarcinoma and use of dental binding domain fusion proteins as targetting inhibitors of dentification, binding domain fusion proteins are search tool for identification, plaque bacteria. GO is useful as a research tool for identification of interacting regulatory proteins. Characterisation and purification of interacting regulators oxidase (GO) The present sequence is Dactylium dendroides galactose oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 QASSYTAPQP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB12928 standard; protein; 639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE12928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galactose oxidase; GO; paper making; aldehyde synthesis; detection; galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; variant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pactylium dendroides galactose oxidase (GO) 7.3.2 variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dactylium dendroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QASSYTAPQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild type Thr substituted with Ser" Misc-difference 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
Key
Misc-difference 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 494
                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162938-A2.
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                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2001.
                                                                                                                                                                                                                                                                                                             25-FEB-2000; 2000US-185001P.
14-FEB-2001; 2001US-0782906.
                                                                                                                                                                                                                                                                              (HERC ) HERCULES INC
                                                                                                                                                                                                                                    Coleman WJ;
                                                                                                                                                                                                                                                    Maffia AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                       Novel variant galactose oxidase enzyme for oxidizing a compound such as guar which is useful in paper making, for enzymatic synthesis of guar which is useful in paper making, the substituted amino alldehydes and pulp biobleaching, has at least one substituted amino
                                                                               Claim 10; Page 46; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 AA;
                                                                                                                                                                                                         2001-648219/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                         Delagrave S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note "wild type Lys substituted with Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.2%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Wild type val substituted with Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild type Cys substituted with Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild type Tyr substituted with His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52; DB 22;
; pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                    Murphy DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                           Rittenhouse Pruss J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                            Bylina E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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25-FEB-2000; 2000US-185001P. 14-FEB-2001; 2001US-0782906.

(HERC ) HERCULES INC.

Delagrave S, Murphy DJ, Rittenhouse Pruss J,

Coleman WJ; Maffia AM,

2001-648219/74.

21-FEB-2001; 2001WO-US05732.

us-09-554-941-2.rag

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The invention relates to variant galactose oxidase (vGO) proteins and their cDNA molecules. Galactose oxidases are useful for oxidising D-galactose side chains of many complex compounds such as guar, major
                                                                                                  Novel variant galactose oxidase enzyme for oxidizing a compound such as aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                   Claim 7; Page -; 65pp; English.
                                                                                                                                                                                                WPI; 2001-648219/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                    Coleman
                                                                                                                                                                                                                                                                     (HERC ) HERCULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy .
                                                                                                                                                                                                                                                                                              14-FEB-2001; 2001US-0782906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC their cDNA molecules, Galactose oxidase (vGO) proteins and CC D-galactose side chains of many complex compounds such as guar, major CC generation of H202 in situ, enzymatic synthesis of aldebydes, pulpe CC prognosis in human colorectal adenocarcinoma and early detection and CC plaque bacteria. Go is useful as a grary detection and CC plaque bacteria. Go is useful as a tragetting inhibitors of Grafical cC characterisation and purification of interacting inhibitors of dental cC crafic and purification of interacting regulatory proteins. CC variant.
                                                                                                                                                                                                                                                                                                                      25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                       WO200162938-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                               Delagrave S, Murphy DJ, Rittenhouse Pruss J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                notem "Wild type Cys substituted with Ser"
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0.82;
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Claim 9; Page -; 65pp; English.
            Novel variant galactose oxidase enzyme for oxidizing a compound such as aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                                                   Maffia AM, ;
Coleman WJ;
                                                                                          WPI; 2001-648219/74.
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14-FEB-2001; 2001US-0782906.
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                                                                                                                                                                                                                                                                                       Misc-difference 494 "Wild type Tyr substituted with Asn"
                                                                                                                                                                                                                                                                                                                     Misc-difference 436
                                                                                                                                                                                                                                                                                                                                               Misc-difference 383
                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            Galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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                                                                                                                  Delagrave S, Murphy DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is not shown in the specification but is ed from Dactylium dendroides galactose oxidase SEQ ID NO: 2
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                                                                                                                                                                                                                                                               /note= "Wild type Val substituted with Ala"
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                                                                                                                                                                                                                                                                                                                                   note= "Wild type Cys substituted with Ser"
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100.0%; Pred. No.
ative 0; Mismatch
                                                                                                         Rittenhouse Pruss J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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RESULT 8
AAE12931
ID AAE1
XX AAE1
XX AAE1
XX AAE1
XX AAE1
XX Gala
KW Gala
KW Mute
XX Synt
XX Dact
OS Synt
XX Misc
FT Misc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plaque bacteria. GO is useful as a research tool for identification, characterisation and purification of interacting regulatory proteins. The present sequence is Dactylium dendroides galactose oxidase (GO)
                                                                                      Maffia AM,
Coleman WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutein; variant
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14-FEB-2001; 2001US-0782906.
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                                                    WPI; 2001-648219/74.
                                                                                                                                         (HERC ) HERCULES INC
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                                                                                                                                                                                                                                                                                                                                                                             ′label= Asn,
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colorectal adenocarcinoma;
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100.0%;
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Pred. No.
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                                                                                                         Rittenhouse Pruss
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0.82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dental plaque; mutant;
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Novel variant galactose oxidase enzyme for oxidizing a compound such guar which is useful in paper making, for enzymatic synthesis of

Novel variant galactose oxidase enzyme for oxidizing a compound guar which is useful in paper making, for enzymatic synthesis of

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RESULT 9
AAE12932
ID AAE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aldehydes and pulp biobleaching, has at least one substituted amino
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                                    WPI; 2001-648219/74.
                                                               Maffia AM,
Coleman WJ;
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14-FEB-2001;
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pulp biobleaching;
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                                                                           Delagrave
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                                                                                                                              2000US-185001P
2001US-0782906
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                                                                                                                                                                                                                                                                               'note= "Wild type Cys substituted with Ser"
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colorectal adenocarcinoma; dental plaque; mutant;
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100.0%; Pred. No. 0.
Live 0; Mismatches
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0.82;
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RESULT 10
AAE12933
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             their cDNA molecules. Galactose oxidases are useful for oxidising D-galactose side chains of many complex compounds such as guar, major glycolipid of human red cells. GO is useful in paper making processes, generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp biobleaching, the use of GO-Schiff's reagent for early detection and prognosis in human colorectal adenocarcinoma and use of GO-glucan binding domain fusion proteins as targetting inhibitors of dental plaque bacteria. GO is useful as a research tool for identification, characterisation and purification of interacting regulatory proteins. The present sequence is Dactylium dendroides galactose oxidase (GO)
         Novel variant galactose oxidase enzyme for oxidizing a compound such guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                         Maffia AM,
Coleman WJ;
                                                                                                                                                                                                                                                                                                                                                                                       Galactose oxidase; pulp biobleaching;
                                                                                                                                                          25-FEB-2000;
14-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Dactylium dendroides galactose oxidase GO.05h1B variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE12933 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The present sequence is not shown in the specification but derived from Dactylium dendroides galactose oxidase SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to variant galactose oxidase (vGO) proteins their cDNA molecules. Galactose oxidases are useful for oxidising
                                                                                                                                (HERC ) HERCULES INC
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2001US-0782906
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                                                                                                                                                                                                                                                                                                                                                                                                      GO; paper making; aldehyde synthesis; detection;
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        Novel variant galactose oxidase enzyme for oxidizing a compound such guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                                    Maffia AM,
                                                                                                                                                       25-FEB-2000;
14-FEB-2001;
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                                                                2001-648219/74
                                                                                                                                                                                                                                                                                                                                                                                                     biobleaching;
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colorectal adenocarcinoma; dental plaque; mutant;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to variant galactose oxidase (vGO) proteins and their cDNA molecules. Galactose oxidases are useful for oxidising D-galactose side chains of many complex compounds such as guar, major glycolipid of human red cells. GO is useful in paper making processes, generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp biobleaching, the use of GO-Schiff's reagent for early detection and prognosis in human colorectal adenocarcinoma and use of GO-glucan binding domain fusion proteins as targetting inhibitors of dental plaque bacteria. GO is useful as a research tool for identification, characterisation and purification of interacting regulatory proteins. The present sequence is Dactylium dendroides galactose oxidase (GO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galactose oxidase; pulp biobleaching;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dactylium dendroides galactose oxidase GO.1h1C variant.
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14-FEB-2001;
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                                           Novel variant galactose oxidase enzyme for oxidizing a compound such guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
                                                                                                       WPI; 2001-648219/74.
                                                                                                                                   Maffia AM,
Coleman WJ;
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 Example 1; Page -; 65pp; English
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2001US-0782906
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colorectal adenocarcinoma; dental plaque; mutant;
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Pred. No.
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0.82;
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                                                                                                                                                                                                                                                                            /note= "Wild type Cys substituted with Ser" Misc-difference 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galactose oxidase; pulp biobleaching;
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                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
Misc-difference 238
                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutein; variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dactylium dendroides galactose oxidase GO8-1h1A variant.
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             WPI; 2001-648219/74.
                                                                                                            25-FEB-2000; 2000US-185001P
14-FEB-2001; 2001US-0782906
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                                       Coleman WJ;
                                                         Maffia AM,
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                                                                                  (HERC ) HERCULES INC
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                                                       Delagrave
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                                                                                                                                                                                                                                          /note= "Wild type Val substituted with Ala"
                                                                                                                                                                                                                                                                   note= "Wild type Tyr substituted with His"
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               Coleman
                                                                                                                                                                                                                                                                     Misc-difference 436
                                                       (HERC ) HERCULES INC
                                                                                     14-FEB-2001;
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                                                                                                                                                                                          WO200162938-A2
                                                                                                                                                                                                                                                                                              Location/Qualifiers Misc-difference 427
                                                                                                                                                                                                                                                                                                                                                                                              Galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; mutant;
                                                                                                                                                                                                                                                                                                                                                       Dactylium dendroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Dactylium dendroides galactose oxidase GO8-1h2A variant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE12937 standard; Protein; 639 AA
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                          Delagrave S,
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2001US-0782906.
                                                                                                                                 2001WO-US05732.
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                                                                                                                                                                                                                                       494
                                                                                                                                                                                                                 /note= "Wild type Val substituted with Ala"
                                                                                                                                                                                                                                               note= "Wild type Tyr substituted with His"
                                                                                                                                                                                                                                                                           note= "Wild type Asn substituted with Thr
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100.0%; Fi
                          Murphy DJ,
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Pred. No.
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                       Rittenhouse Pruss J,
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                             WPI; 2001-648219/74
                                                                                                                                                                                                                                       25-FEB-2000; 2000US-185001P
14-FEB-2001; 2001US-0782906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dactylium dendroides. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-galactose side chains of many complex compounds such as guar, major glycolipid of human red cells. GO is useful in paper making processes, generation of H2O2 in situ, enzymatic synthesis of aldehydes, pulp biobleaching, the use of GO-Schiff's reagent for early detection and prognosis in human colorectal adenocarcinoma and use of GO-glucan binding domain fusion proteins as targetting inhibitors of dental plaque bacteria. GO is useful as a research tool for identification, characterisation and purification of interacting regulatory proteins. The present sequence is Dactylium dendroides galactose oxidase (GO)
                                                                                    Coleman WJ;
                                                                                                                     Maffia AM,
                                                                                                                                                                                                                                                                                                                                      21-FEB-2001; 2001WO-US05732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galactose oxidase; GO; paper making; aldehyde synthesis; detection; pulp biobleaching; colorectal adenocarcinoma; dental plaque; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE12939;
                                                                                                                                                                                (HERC ) HERCULES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200162938-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutein; variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variant galactose oxidase enzyme for oxidizing a compound such as guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino
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                                                                                                                  Murphy DJ,
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                              Note: The present sequence is not shown in the specification but is derived from Dactylium dendroides galactose oxidase SEQ ID NO: 2 shown in page 10 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel variant galactose oxidase enzyme for oxidizing a compound such as guar which is useful in paper making, for enzymatic synthesis of aldehydes and pulp biobleaching, has at least one substituted amino acid -
                                                                                                                                                                                                                                                                                    Sequence
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| 147 QASSYTAPQP 156
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                                                                                                                                                                                                                                                                                      639 AA;
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Maximum DB seq length: 2000000000
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57
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1: sp_archea:*
2: sp_bacteria:
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
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5: sp_mammal:*
6: sp_mammal:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                           sp_rodent:*
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sp_archeap:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 4 4 4 6 6 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result
40 39 39 39 38 38 38 37 37 37 37 37	Score
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6 O9RU88 13 O9RS17 20 O98S16 3 O98S16 3 O996N4 11 O90457 11 O90494 11 O8VDM6 4 P78364 4 P78364 4 P7837 5 O61711 5 O61711 3 O9P5NO 12 O91488	;
Qgru88 deinococcus Qgsal7 xenopus lae Q98s16 xenopus lae Q98s16 xenopus lae Q98s16 xenopus lae Q99s16 xenopus lae Q99s17 gallid herp Q9453 hevea brasi Q8vdm6 mus musculu p78364 homo sapien Q9rwz8 deinococcus Q9rwz8 deinococcus Q9rwz8 tohizosacch Q9xe77 sorghum bic Q61711 caenorhabdi Q95500 schlzosacch Q91hs8 tt virus. o	Description Q8wp81 caenorhabdi
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	)54919 )9YVZ0 )9YVZ0 )9XCK3 )9XCK3 )02XG5 (09XH15 (09XH15 (09XH15 (09XH15 (09XH15 (09XH17 (09X
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	Q54919 Q54920 Q9vv20 Q9v20 Q9sm1 Q9sm1 Q8ygx Q9sm3 Q9xu3 Q9xu3 Q9xu3 Q9yx Q9963 Q9963 Q9963 Q9963 Q9963 Q9963 Q910 Q911 Q9963 Q911 Q9963 Q911 Q9963 Q911
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	streptocoo drosophila streptococ ceratitis ceramics brucella caenorhabd frhizobium muscu brachydae frhizobium muscu brachydae homo sapic homo sapic homo sapilus gillassa gillassa gillassa gillassa gillassa gillassa gillassa gillassa gillassa gillassa gillassa drosophil
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Wild A.; (APR-1996) to the EMBL/GenBank/DDBJ databases. 

BLDmitted (6PR-1996) to the EMBL/GenBank/DDBJ databases. 

EMBL; Z70688; CAD21656.1; -... 

EMBL; Z70683; CAD21656.1; -... 

EMBL; Z70683; CAD21626.1; -... 

EMBL; Z70686; CAD21626.1; -... 

EMBL; Z70683; CAD21626.1; -... 

EMBL; Z70686; C
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
MCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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RESULT Q9RU88

Matches

Indels

0,

Gaps

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Query Match
                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Eyes absent-1 alpha.
Xenopus Laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                MEDLINE=21233041; PubMed=11335132;
David R., Ahrens K., Wedlich D., Schlosser G.,
"Xenopus Eyal demarcates all neurogenic placodes as well as migrating
hypaxial muscle precursors.";
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome.
SEQUENCE 224 AA; 25032 MW; 05CC3BDF11281B35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001268; Complex1_30K, Pfam; PF00329; complex1_30Kd; 1. Probom; PD001581; Complex1_30K; 1. PROSTIE; PS00542; COMPLEXI_30K; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wakarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001994; AAF11071.1; -.
TIGR; DR1504; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    3 SSYTAPQPQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NADH dehydrogenase I, C subunit.
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7; Conserv
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77.88;
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77.8%;
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Pred. No. 15;
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                                                                                                                                                                                                                                                                          587 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                          Q9P6N4
                                                                                                                                                                                                                                                                                                                                                       RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                               γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
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DR
SQ
                                                                                                                    STRAIN-972H-;
                                                                                                                                                                         Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                            Q9P6N4;
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                Putative vacuolar biogenesis protein, yeast endl homolog.
                                                                                                                                                                                                                                               01-OCT 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pavid R., Ahrens K., Wedlich D., Schlosser G.;
"Xenopus Eyal demarcates all neurogenic placodes as well as migrating hypaxial muscle precursors.",
Mech. Dev. 103:189-192(2001).
EMBL; AF352029; AAK31355.1;
EMBL; FFFO; IPR001454; Hlgnase/hydrlase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPROVITED Pfam; PE00702; Hydrolase; PE0070E 592 AA; 64640
                                                                                                                                                                                                                                                                                                                                                                                             167 SSFTAPQP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21233041; PubMed=11335132; David R., Ahrens K., Wedlich D., S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q98SL6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                         3 SSYTAPQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mech. Dev. 103:189-192(2001).
EMBL; AR552028; AAK31354.1;
InterPro: IPR001444; Hlynase/hydrlase.
Pfam; PF00702; Hydrolase; 1.
SEQUENCE 587 AA; 64142 MW; 5EE9813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 SSFTAPQP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SSYTAPOP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64640 MW; 84BEE3996231B2C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.4%; Score 39; DB
87.5%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64142 MW; 5EE9813F6075ADE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.4%; Score 39; DB
87.5%; Pred. No. 44;
                                                                                                                                                                                          Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                             906 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 587;
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Q98SL7 RESULT 3

Q98SL7; Q98SL7 밁 δÃ

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290H57
ID 099H
AC 099H
AC 099H
DT 01-+--
DT 01----
DT 01---

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9OH57 PRELIMINARY:
O9OH57: O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 SYTAPSPQ 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "sequence of the infectious laryngotracheitis virus (SA-2 strain) unique long region UL28 to UL43."; submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF168792; AAD55207.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alphaherpesvirinae; Infectious laryngotracheitis-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallid herpesvirus 1.
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q949Н3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SYTAPQPO 11
                                                                                                                                                                                                                                                                                                                                                                                                                             Hevea brasiliensis (Para rubber tree).
Bevea brasiliensis (Para rubber tree).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; Rosic
Spermatophyta; Magnoliophyta; eudicottyledons; core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putative class I chitinase (Fragment).
                                                                                                                                                                                                                                                          O'Riordain G., Godnic-Cvar J., Radauer C., Hoffmann-Sommergruber K., Scheiner O., Ebner C., Breiteneder H.; "Cloning and expression of a class I chitinase from latex, Hevea
                                                                                                                                                                                                                                                                                                                                                                                                        eurosids I; Malpighiales; Euphorbiaceae; Hevea
                                                                                                                                                                                           Pfam; PF00187; Chitin_bind_1; 1.
pfam; PF00182; Glyco_hydro_19; 1.
proDom; PD000574; Glyco_hydro_19; 1.
pROSITE; PS00773; CHITINASE_19_1; UNKNOWN_1.
pROSITE; PS00774; CHITINASE_19_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3981;
                                                                                                                                         Interpro; IPR001002; Chitin_binding_1.
Interpro; IPR000726; Glyco_hydro_19.
  Chitin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QASSYTAPQPQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QSNSHSTPQPQ 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.7%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38;
pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosidae;
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P78364
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021506; AAH21506.1; -.
InterPro; IPR003034; SAP.
InterPro; IPR003878; SPRY_domain.
InterPro; IPR003877; SPRY_receptor.
InterPro; IPR003877; SPRY_receptor.
InterPro; IPR003871; SPRY_receptor.
InterPro; IPR003871; SPRY_receptor.
SMARP; SM00513; SAP; 1.
SMARP; SM00513; SAP; 1.
SMARP; SM00513; SAP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similar to E1B-55 kDa-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8VDM6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8VDM6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 QASSYCSPSP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QASSYTAPQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
polyhomeotic 1 homolog (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P78364;
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=97220024; PubMed=9121482;

MEDLINE=97220024; PubMed=972200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 SSYTPPQP 758
                    MO1. Cell. Biol. 17:2326-2335(1997).

EMBL; U89277; AAC51169.1; -.

Interpro; IPR001660; SAM.

Pfam; PF00336; SAM; 1.
                                                                                                            vertebrate polycomb-group protein BMI1 and human homologs polyhomeotic.
                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 7; Conserv
  SMART; SM00454; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 SSYTAPOP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
295 AA; 31647 MW; 6B748B2E3BBFCF96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   859 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 11
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              859 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1004 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11; Length 859;
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RESULT 11
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AC Q8YEW
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DE POtas
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OC BACCE
OC BA
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Q9RWZ8
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STRAIN-16M / ATCC 23456 / BIOTYPE 1;
MEDLINB=20020109; PubMed=11756688;
DelVecchio v.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                            Brucella melitensis
                                                                                                                                                                                                                                                                                                                            Potassium efflux system protein PHAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8YBW7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiodurans R1.";
Science 286:1571-1577(1999).
Science 286:01910; AAF10097.1;
TIGR; DR0517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 ASSNTAPAPQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein DR0517.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ASSYTAPOPO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8948 MW;
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DE
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F6DDB1AB9F1FDE5D CRC64;
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Pred. No. 1.2e+02;
2; Mismatches 1
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Patatin-like protein.
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl.
                                                                                                                                 Q9XE77;
                                                                                                                                              Q9XE77
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                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                  "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GPP-fusion genomic DNA library."; EMBL; AB027821; BAA87125.1; -
                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00664; ABC_membrane;
                                                                                                                                                                                                           73 SSYTSPNPE 81
                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001140; ABCtranprtrTM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hiraoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20223868; PubMed=10759889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 16.6 kDa protein (Fragment).
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomycetales; Schizosaccharomycetaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UU44
                                                                                                                                                                                                                                     3 SSYTAPQPQ 11
                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brucella melitensis.",
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE00971; AAL54011.1;
InterPro; IPR002757; DUF67,
Pfam; PF01898; DUF67, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 112 AA; 12010 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD006097; DUF67; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N., Overbeek R.; "The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 QAAQYTDPVPQ 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QASSYTAPQPQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                             6;
                                                                                                                                                                                                                                                                                                  142 142
142 AA; 16561 MW; 8296B1B8BD0B5C4F CRC64;
                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                     64.9%; Score 37; DB 66.7%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.9%; Score 37; DB 63.6%; Pred. No. 16;
                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D386BE189F5EE81B CRC64;
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                                                                                                                                 422 AA.
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                                                                                                                                                                                                                                                                           DB 3; Length 142;
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                 Poaceae; PACC clade;
                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                              Gaps
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RESULT 14
061711
1D 06171
AC 06171
DT 01-AU
DT 01-JU
DT 0
RESULT 15
Q9P5N0
ID Q9P5N
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Best Local 9
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                                                                                                                                                                                                                                                                             Query Match
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 64.6 kDa protein.
R119.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            061711
061711;
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"Microsynteny analysis of 22-kba zein cluster in maize and sorghum.";
submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061282; AAD22169.1; -
InterPro; IPR002641; Patatin.
Pfam; PF01734; Patatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF063007; AAC16433.1; -.
Interpro; Ipr000504; RNA_rec_mot.
Pfam; PF00076; rrm; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clarke K., Bauer C., O'Neal D.;
"The sequence of C. elegans cosmid R119.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
     Q9P5N0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             investigating biology. The C Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                               Hypothetical protein SEQUENCE 583 AA; (
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50102; RRM; 1.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                              125
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                                                                                                                                                                                                                           Local Similarity tes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QASSYTAPQ 9
                                                                                                                                                                              1 QASSYTAPQPQ 11
                                                                                                                              QASSYLPPNPR 135
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                                                                                                                                                                                                                                Conservative
     PRELIMINARY;
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77.8%;
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Pred. No. 73;
0; Mismatches
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Pred. No. 1e+02;
1; Mismatches
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     PRT;
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     1465 AA
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73;
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279 SSYTSPNPE 287

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                     Query Match
Best Local S
Matches 6
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Probable ATP-dependent permease c359.05.
SPBC359.05.
                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PDUUUVVV,
SMART; SM00382; AAA; 1.
SMART; SM00381; ABC_TRANSPORTER;
DROSITE; PS00211; ABC_TRANSPORTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                 NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00664; ABC_membrane; Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                        SEQUENCE
                                                                 CARBOHYD
                                                                                                                            TRANSMEM
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3 SSYTAPQPQ 11
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                     Similarity 6; Conserv
                                                                                                  940
961
1034
1055
1134
1155
                                                                         614
1260
346
                     Conservative
                                                                                                                                                                                                                                                                                                                                                )211; ABC_TRANSPORTER; 2.
protein; ATP-binding; Transmembrane; Glycoprotein;
                                                         ĀΑ;
                                                               1076
                                                                                                           64.98;
66.78;
                                                         166612
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                       2;
                       Score 37; DB
Pred. No. 2.9e
2; Mismatches
                                                         Ψ,
                                                                                                                                                                                               7 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
8 (BY SIMILARITY)
                                                                                                                                                                                                                                  5 (BY SIMILARITY).

CYTOPLASMIC (BY SIMILARITY).

6 (BY SIMILARITY)
                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
M; B15F1579B0895332 CRC64;
                                                                                EXTRACELLULAR (BY SIMILARITY)
13 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
ATP (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                    10 (BY SIMILARITY).
EXTRACELLULAR (BY SIMILARITY).
11 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
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9 (BY SIMILARITY).
CYTOPLASMIC (BY SIMILARITY).
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5 (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
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2 (BY SIMILARITY).
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7 (BY SIMILARITY).
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                                                                                                                              (BY SIMILARITY)
                                          DB 3;
                                9e+02;
                                        Length 1465;
                         Indels
                         0,
                        Gaps
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Search completed: January 13, 2003, 09:59:45 Job time: 44.7436 secs

SMART; SM00231; E Oxidoreductase; S SIGNAL CHAIN 1 REPEAT 279 REPEAT 279 REPEAT 323

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GALACTOSE OXIDASE. KELCH 1. KELCH 2. KELCH 3.

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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                           Query Match
                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics are not restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
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EMBL; AK001743; BAA91875.1; --
EMBL; AK022781; BAB14244.1; --
EMBL; AK022782; BAB14243.1; --
EMBL; BC008082; AAH08082.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 2. SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00678; WD_REPEATS_1; 2. PROSITE; PS50082; WD_REPEATS_2; 5. PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00400; WD40; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001680; WD40.
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                                                                                                                                                                                                                       CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat; WD repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                  VARIANT
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                                                                                                                                                                                                    SEQUENCE
                                                                                                                        Local Similarity
  89 YTAPQPE 95
                                                   5 YTAPQPQ 11
                                                                                                                                                                                                      423 AA;
                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                             286
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                                                                                                                                 64.9%;
85.7%;
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E -> G.
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Y -> C.
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                                                                                                                                 Score 37; DB pred. No. 19;
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L -> M (IN REF.
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                                                                                                                                                                                                            6D088C640AC981D8 CRC64;
                                                                                                              Mismatches
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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S., RA Arzakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., RA Kudota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Sasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kombaerts P., RA Gustincich S., King B., Ringwald M., Radriguez I., Sakamoto N., RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Sasaki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Havashiraki Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JJA4; Q9JKF5; Q9CST3;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WD-repeat protein 12 (YTM1 homolog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nal B., Mohr E., Da Silva M.I., Tagett R., Navarro C., Carroll Depetris D., Verthuy C., Jordan B.R., Ferrier P.; Wdr12, a mouse gene encoding a novel WD-repeat protein with a motchless-like amino-terminal domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WDRC_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 79:77-86(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21686157; PubMed=11827460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            made by oligo-capping method.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hashimoto K.;
"isolation of full-length cDNA clones from mouse brain cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osada N., Kusuda J., Tanuma R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mouse homologue of Saccharomyces cervisiae YTM1."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/SVJ X C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Testis, and Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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                                                                                                                                                                             Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
                                                                                                                                                                                                                                                                                       Nature 409:685-690(2001).
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 423 AA.
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STRH
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   the European Bioinformatics Institute.
      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                    -I- FUNCTION: PROBABLY IS A DIHYDROSTREPTOSYL GLYCOSYLTRANSFERASE, INVOLVED IN THE FIRST GLYCOSYLATION STEP CONDENSING STREPTIDINE-6-PHOSPHATE AND DIHYDROSTREPTOSE (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: dippl-L-dihydrostreptose + streptidine 6-
                                                                                                                                    Mansouri K., Piepersberg W.;
"Genetics of streptomycin production in Streptomyces griseus:
nucleotide sequence of five genes, strFGHTK, including a phosphatase
                                                                                                                                                                            MEDLINE=91375432; PubMed=1654502;
                                                                                                                                                                                                                                                                         dihydrostreptose-streptidine-6-phosphate dihydrostreptosyltransferase (EC 2.4.2.27).
                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                           Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                   Bacteria;
                                                                                                                                                                                                                                                          Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                      STRH_STRGR
P09399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00678; WD_REPEATS_1; 2.
PROSITE; PS50082; WD_REPEATS_2; 5.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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99
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ProDom; PD000018; WD40; 2.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001680; WD40. Pfam; PF00400; WD40; 7.
                                            PATHWAY: Streptomycin biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC004748; AAH04748.1; -...
MGD; MGI:1927241; Wdr12.
                                                                                                                                                                                                                                                                                                                                                                                                  89 YTAPQPE 95
                                                            phosphate = dTDP + O-1/4-alpha-L-dihydrostreptosyl-streptidine
                                                                                                                                                                                                                                                                                                                                                                                                                      5 YTAPQPQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                        Gen. Genet. 228:459-469(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK016611; BAB30336.1; -.
                                                                                                                                                                                                                                    Actinobacteria; Actinobacteria (class); Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 AA;
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187
255
295
340
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                         PRT;
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T -> A (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WD 1.
WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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                                                                                                                                                                                                                                                                                                                                         384 AA.
 There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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restrictions
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RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Buck D., Burrill W.D., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G.P., Carder C., Carter N.P.,
RA Chegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Cling S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Hummond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.M., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rice C.M., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CP24_HUMAN
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                         "The DNA sequence and comparative analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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007973; Q15807;
01-OCT_1996 (Rel. 34, Created)
16-OCT_2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450-CC24, mitochondrial precursor (EC 1.14.-.-) (P450-CC24) (Vitamin D(3) 24-hydroxylase) (1,25-dihydroxyvitamin D(3) 24-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-21638749; PubMed-11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93281615; PubMed=8506296;
Chen K.-S., Prahl J.M., Deluca H.F.;
"Isolation and expression of human 1,25-dihydroxyvitamin D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:4543-4547(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Y00459; CAA68520.1; -. PIR; S17778; S17778. Streptomycin biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.2%; Score 36; 70.0%; Pred. No.

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycosyltransferase
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TRA_BPMU
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DT 01-A
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen K.-S., DeLuca H.F.; "Cloning of the human 1 alpha, 25-dihydroxyvitamin D-3 24-hydroxylase gene prometer and identification of two vitamin D-responsive
                                                        P07636: P06021;
01-APR-1988 (Rel. 07, Created)
01-FEB-1996 (Rel. 33, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S67623; AAB29308.1; HSSP; P14779; 1JPZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maps to a different chromosomal location than that
D-deficient rickets.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1263:1-9(1995).
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                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bone Miner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 258-514 FROM N.A.
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                Bacteriophage Mu.
                               A OR 3
                                           Transposase
                                                                                                                 TRA_BPMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion;
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 Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                          Local Similarity es 5; Conserv
                                                                                                                                                                                                                 2 ASSYTAPOPO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SONE MINER. RES. 8:1397-1406(1993).
FUNCTION: HAS A ROLE IN MALNTAINING CALCIUM HOMEOSTASIS. CATALYZES THE MADPH-DEPENDENT 24-HYDROXYLATION OF 25-HYDROXYVITAMIN D(3) IN THE PRESENCE OF ADRENODOXIN AND NADPH-ADRENODOXIN REDUCTASE.
                                                                                                                                                                                       STAYTSPQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U60669; AAB03776.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          case;
                                                                                                                                                                                                                                              Conservative
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                                                                                                                 STANDARD;
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    13, Last sequence update)
    40, Last annotation update)

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462
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50.0%;
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 no
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 RNA stage; Caudovirales; Myoviridae;
                                                                                                                                                                                                                                                                                                                HEME (POTENTIAL).
G -> A (IN REF. 1).
AY -> V (IN REF. 1).
D -> G (IN REF. 1).
V -> R (IN REF. 1).
A -> E (IN REF. 1).
S -> G (IN REF. 1).
S -> G (IN REF. 4).
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                                                                                                                                                                                                                                                                        Score 36;
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Clubb R.T., Schumacher S., Mizuuchi K., Gronenborn A.M., "Solution structure of the I gamma subdomain of the Mu ev DNA-binding domain of phage Mu transposase."; J. Mol. Biol. 273:19-25(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel class of winged helix-turn-helix protein: the DNA-binding domain of Mu transposase."; Structure 2:1041-1048(1994).
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Morgan G., Hatfull G., Hendrix R.;

Morgan G., Hatfull G., Hendrix R.;

"Genome of bacteriophage Mu and comparison with the Haemophilus

influenzae Mu-like prophage FluMu.";

submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE BY NMR OF 173-247.
MEDLINE=98035037; PubMed=9367742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gronenborn A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95187707; PubMed-7881904; Clubb R.T., Omichinski J.G., Savi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=83218562; PubMed=6222246; Toussaint A., Faelen M., Desmet L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Priess H., Kamp D., Kahmann R., Braeuer B., Delius H.; "Nucleotide sequence of the immunity region of bacteriophage Mol. Gen. Genet. 186:315-321(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-88 FROM N.A. MEDLINE=83012203; PubMed=6214696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Priess H., Brauer B., Schmidt C., Kamp D.;
"Sequence of the left end of Mu.";
(In) Symonds N., Toussaint A., van de Putte P., Howe
Phage Mu, pp.277-296, Cold Spring Harbor Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                        structural motif for DNA transposition and retroviral integration.";
                                                                                                                                                                                                                                 Rice P., Mizuuchi K.;
"Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bacteriophage Mu transposase core: a common "Structure" of the bact
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New York (1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Solution structure of the Mu end DNA-binding phage Mu transposase: modular DNA recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98070329;
                                              1 82:209-220(1995).

FUNCTION: THIS TRANSPOSASE IS ESSENTIAL FOR INTEGRATION, REPLICATION-TRANSPOSITION, AND EXCISION OF MU DNA.

MISCELLANEOUS: MU CAN TRANSPOSE ITS DNA INTO MULTIPLE SITES IN MANY BACTERIAL GENOMES AND MEDIATE A VARIETY OF DNA MANY BACTERIAL GENOMES AND MEDIATE A VARIETY OF DNA REARRANGEMENTS. TRANSPOSASE (ENCODED
  MISCELLANEOUS:
                       BY GENE A) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9405381;
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TRANSPOSITION ENHANCER (ENCODED UNLIKE OTHER TRANSPOSONS MU HAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cai M., Mizuuchi K., Clore G.M.,
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Best Local
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16-OCT-2001
16-OCT-2001
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                                  Kappeler S., Farah Z., Puhan Z.;
"Sequence analysis of Camelus dromedarius milk caseins.";
J. Dairy Res. 65:209-222(1998).
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR004189; Mu_transposase.
Pfam; PF02316; Mu_DNA_bind; 1.
Pfam; PF02914; Mu_transposase; 1.
Pransposition; Transposable element; DNA-binding; DNA excision;
                                                                                                                                    MEDLINE=98291310; PubMed=9627840;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        NCBI_TaxID=9838;
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A_BIND 35 5
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SIMILARITY: STRONG, TO H.INFLUENZAE HI1478.
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2EZI;
2EZK;
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14-JAN-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 40, Created)
(Rel. 40, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            precursor.
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IMPORTANT ROLE IN DETERMINATION OF THE SURFACE
                                                                                                                                                                   TISSUE=Mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408
75003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409
66
                                                                                                                                                                                                                                                                                                 (Dromedary) (Arabian camel).
Chordata; Craniata; Vertebrata; Eutel
Cetartiodactyla; Tylopoda; Camelidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombination; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H-T-H MOTIF (POTENTIAL).
H-T-H MOTIF (POTENTIAL).
G -> R (IN REF. 5).
                                                                                                                                                                   gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B882CFDCBFC0B2E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> R (IN REF. 5).
-> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ψ
                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Mooney R., Moule S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Squares D., Seeger K., Sharp S.,
RA Skilton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Skilton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
Borzym K., Lanyc.
Borzym K., Lanyc.
Eger P., Zimmermann W., wec..
Eger P., Zimmermann S., '
Goffeau A., Cadieu E., Dreano S., '
Goffeau A., Cadieu S.J., Xiang Z.,
Thert F., Aves S.J., Xiang Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                059683;
15-DEC-1998 (Rel. 37, Cr
15-DEC-1998 (Rel. 37, La
15-JUN-2002 (Rel. 41, La
Translation initiation f
                                                                                                                                                                                                                                                                                                                             Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IF-2(Mt)).
SPBC2F6.01 OR SPBC1271.15C.
Schizosaccharomyces pombe (Fis
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ012630; CAA10079.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPERTIES OF THE CASEIN MICELLES (BY SIMILARITY).
-:- SUBCELLULAR LOCATION: EXTRACELLULAR.
-:- TISSUE SPECIFICITY: MAMMARY CLAND; MILK.
-:- SIMILARITY: BELONGS TO THE BETA-CASEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDKIYTFPQPQ 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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37, Created)
37, Last sequence update)
41, Last annotation update)
ation factor IF-2, mitochondrial precursor (IF-2Mt)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fission yeast).
ota; Schizosaccharomycetes;
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Pred. No.
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HOSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
HOSPHORYLATION (BY SIMILARITY).
AOF9F41D2EA7C518 CRC64;
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RESULT 9
FLNA_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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InterPro; IPR000795; EF_GTPbind.
InterPro; IPR000178; IF2.
InterPro; IPR005225; Small_GTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AL034353; CAA22205.1; --
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Pfam; PF03144; GTP_EFTU_D2; 2.
ProDom; PD186100; IF2; 1.
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                                                                                                                                                                                                                                                                                01-MAY 1991 (Rel. 18, Created)
01-MAY 1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 18, Created)
15-JUN-2004 (Rel. 18, Created)
15-JUN-2004 (Rel. 18, Created)
15-JUN-2004 (Rel. 18, Last sequence update)
15-JUN-2004 (Rel. 18
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SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE IF-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUNCTION: IF 2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION PUNCTION: IS SYNTHESIS. PROTECTS FORMYLMETHIONYL-TRNA FROM FOR PROTECT SYNTHESIS. PROTECTS FORMYLMETHIONYL-TRNA FROM SPONTANEOUS HYDROLYSIS AND PROMOTES ITS BINDING TO THE 30S SPONTANEOUS HYDROLYSIS AND PROMOTES IN THE HYDROLYSIS OF GTP RIBOSOMAL SUBUNITS. IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GTP RIBOSOMAL SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 EAAAYSAPSPK 158
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90361737; PubMed=2391361;
MEDLINE=90361737; PubMed=2391361;
Gorlin J.B., Yamin R., Egan S., Stewart M., Stossel T.P.,
Gorlin J.B., Yamin R., Egan S., Stewart M., Stossel T.P.,
Kwiatkowski D.J., Hartwig J.H.;
Kwiatkowski D.J., Hartwig J.H.;
Human endothelial actin-binding protein (ABP-280, nonmuscle
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QASSYTAPQPQ 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G-DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 2647 AA
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filamin): a molecular leaf spring.";
J. Cell Biol. 111:1089-1105(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96311563; PubMed=8733135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G6PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1658-1772 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mapping of two genes encoding isoforms of the actin binding protein ABP-280, a dystrophin like protein, to Xq28 and to chromosome 7."; hum. Mol. Genet. 2:761-766(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93357748; PubMed=7689010;
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Repetto M., Villa A., Frattini A., Zoppe M., Vezzoni P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stossel T.P., Condeelis J., Cooley L., Hartwig J.H., Noegel A., Schleicher M., Shapiro S.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sheen V.L., Dixon P.H., Fox J.W., Hong S.E., Kinton L., Sisodiya S.M., Buncan J.S., Dubeau F., Scheffer I.E., Schachter S.C., Wilner A., Buncan J.S., Dubeau F., Scheffer I.E., Schachter S.C., Wilner A., Henchy R., Crino P., Kamuro K., DiMario F., Berg M., Kuzniecky R., Henchy R., Crino P., Kamuro K., DiMario F., Berg M., Kuzniecky R., Cole A.J., Bromfield E., Biber M., Schomer D., Wheless J., Silver K., Cole A.J., Bromfield E., Biber M., Schomer D., Wholess J., Silver K., Mochida G.H., Berkovic S.F., Andermann F., Andermann E., Dobyns W.B., Woodl N.W., Walsh C.A., Walsh C.A.,
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Nat. Rev. Mol. Cell Biol. 2:138-145(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS PH PHE-656 AND THR-1764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nodular heterotopia in males as well as in females.";
Hum. Mol. Genet. 10:1775-1783(2001).
-i- FUNCTION: Promotes orthogonal branching of actin filaments and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        links actin filaments to membrane glycoproteins. Anchors various transmembrane proteins to the actin cytoskeleton and serves as a scaffold for a wide range of cytoplasmic signaling proteins. SUBGUNIT: Homodimer. Interacts with cvHsp. Interacts with various other binding partners in addition to filamentous actin. SUBGELLULAR LOCATION: PERIPHERAL CYTOPLASM.
                                                                                                                                                                                                                                                                                             PIM: The Nefects in FLMA are the cause of periventricular DISEASE. Defects in FLMA are the cause of periventricular DISEASE. Defects in FLMA are the cause of periventricular (PH) also called nodular heterotopia (PH) also called nodular heterotopia (PH) also called nodular heterotopia (PH). PH is an X-linked developmental periventricular (NHBP or BENHI). PH is an X-linked developmental dominant disorder in which many neurons fail to migrate into the disorder in which many neurons fail to migrate into the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular programments of the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cortex. They remain as nodules lining the ventricular cerebral cerebral cortex. They remain as nodules lining the ventricular cerebral cerebral
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                                                                                                        expressing cells.
SIMILARITY: THE ACTIN-BINDING DOMAIN IS OF A TYPE FOUND IN MANY SIMILARITY: THE ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN, ACTIN-BINDING PROTEINS (SUCH AS ACTININ, DYSTROPHIN, FIMBRIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet. 5:659-668(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION EXTENT CHANGES IN RESPONSE TO CELL
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PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
PROSITE; PS50194; FILAMIN REPEAT; 24.
                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00307; CH; 2.
Pfam; PF00630; Filamin; 24.
SMART; SM00033; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                    Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001589; Actbind_actnin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A37098; A37098.
HSSP; P13466; 1KSR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP-120, ABP-180, OR BETA-FODRIN).
-i- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.
-i- SIMILARITY: CONTAINS 24 FILAMIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w; HGNC:3754; FLNA.
300017;
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L44140; AAA92644.1;
X70082; CAA49687.1;
X70085; CAA49690.1;
                656
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1155
1250
1350
1443
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1950
2039
2131
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1539
1636
1740
1778
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FILAMIN 17.
FILAMIN 18.
FILAMIN 19.
FILAMIN 20.
FILAMIN 21.
FILAMIN 22.
FILAMIN 23.
/FTId=VAR_012834.
                                                           CLEAVAGE (BY CALPAIN).
V -> A (IN DBSNP:1064816).
                 /FTId=VAR_012833.
                                                                             SELF-ASSOCIATION SITE, TAIL
                                    /FTId=VAR_012832
                                                       /FTId=VAR_012831
                                                                                             FILAMIN 24
                                                                                                                                                                                                                  FILAMIN 10.
FILAMIN 11.
FILAMIN 12.
FILAMIN 13.
                                                                                                                                                                                          HINGE
                                                                                                                                                                                                FILAMIN 15
          -> F (IN PH)
                         -> A (IN DBSNP:730319).
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                                          (IN DBSNP:1064817).
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ID PRAA_STRCO
AC PS473a),
DT 01-OCT-
DT 15-UNM-
GN PKAA OF
ON STRAIN-
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DR SMART;
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                       Phossite; P54739; ...
Interpro; IPR000719; Euk_pkinase.
Interpro; IPR002709; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
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HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                       EMBL; D86821; BAA13168.1; -.
                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com-
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Nature 417:141-147(2002).
-!- PTM: AUTOPHOSPHORYLATED MAINLY AT THR AND SLIGHTLY AT SER.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-1964(10) PubMed=12000953;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urabe H., Ogawara H.; "Cloning, sequencing and expression of serine/threonine kinase-encoding genes from Streptomyces coelicolor A3(2)."; Gene 153:99-104(1995).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine/threonine protein kinase pkaA (EC 2.7.1.-)
PKAA OR SCC2974 OR SCE50.02C.
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2647 AA;
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H -> D (IN REF. 2).
MW; 6C1A07041DFA3D42 CRC64;
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PROSITE; PS00108; PROTEIN\_KINASE\_ST;

M00220; S\_INC, 1.
PS00107; PROTEIN\_KINASE\_ATP; F

FALSE\_NEG

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEA_HPV54 STANDARD;
Q81022;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way used and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable E4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 437 QPQRYATPQPQ 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=37113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Papillomavirus
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                          EMBL; U37488; AAA79191.1; -
InterPro; IPR003861; Papill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QASSYTAPQPQ 11
                     Cancer pagurus (Rock crab).

Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;

Bukaryota; Bucarida; Decapoda; Pleocyemata;

Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata;
                                                                                                                                       CANPG
                                                          P81584;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
cuticle protein CP1876 (CPC1876).
NCBI_TaxID=6755;
             Brachyura;
                                                                                                                                                                                      96 QTSNHTAPQ 104
                                                                                                                                                                                                                                  Local Similarity
es 6; Conserv
                                                                                                                                                                                                             1 QASSYTAPQ 9
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6; Conserva
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                                                                                                                            CANPG
                                                                                                                                                                                                                                                                                                     protein
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48
142
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301
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                                                                                                                                                                                                                                                                                       134 AA; 15373 MW; B157979B6035EE2A CRC64;
             Eubrachyura; Cancroidea; Cancridae; Cancer
                                                                                                                                                                                                                                        Conservative
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142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                Papilloma_E4.
                                                                                                                                                                                                                                                       57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no RNA stage; Papillomaviridae;
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ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence update)
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Pred. No.
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                                                                                                                                                                                                                                                         Score 33; DB
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                                                                                                                                    175 AA
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Comp. Biochem. Physiol. 123A:203-211(1999).
-i- TISSUE SPECIFICITY: CALCIFIED SHELL.
-i- MASS SPECTROMETRY: MW-18759.8; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99354472; PubMed=10425740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9419428; PubMed-8145851;
Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S.,
Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J.,
Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
Duda G., Martina N., Peterson D., Hennick D., Roncarolo M.G.,
Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G.,
Muench M., Kosnet O., Dubreuil P., Birnbaum D., Lee F.;
Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.;
Talgand for FLT3/FIK2 receptor tyrosine kinase regulates growth of
"Ligand for FLT3/FIK2 receptor tyrosine kinase regulates growth of
haematopoietic stem cells and is encoded by variant RNAs.";
Nature 368:643-648(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P49771;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FL3L_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ligand) (Flt3L).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                       Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J., "Cloning of the human homologue of the murine fit3 ligand: a growth factor for early hematopoietic progenitor cells.";
                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94235842; PubMed=8180375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 ADVYTMPRPQ 52
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                                                                                                                                                                                                                                                                                                           Blood 83:2795-2801(1994).
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                          "Structural analysis of human and murine flt3 ligand genomic loci."; oncogene 11:1165-1172(1995).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
            bundles and cystine knots.

Nat. Struct. Biol. 7:486-491(2000).

Nat. Struct. Biol. 7:486-491(2000).

-i. FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING FACTORS AND INTERLEUKINS.

FACTORS AND INTERLEUKINS.
                                                                                                                                                                                                                                                             MEDLINE-96032581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ASSYTAPOPO 11
                                                                                                                                                                                                                                            Lyman S.D., Stocking
                                                                                                               Savvides S.N., Boone T., Karplus P.A.; "F1t3 ligand structure and unexpected commonalities of helical
                                                                                                                                            MEDLINE=20343011; PubMed=10881197;
                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 SUBCELLULAR LOCATION: Type I membrane protein (isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuticle
                                                                                                                                                                                                                                                                   PubMed=7566977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.9%;
                                                                                                                                                                                                                                                 K., Davison B., Fletcher F., Johnson L.,

    Mismatches

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Pred. No.
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Matches
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
                                                                     Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S., "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.", Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                     10 'OCT'-2001 (Rel. 40, Last annotation update)
Putative outer membrane protein CPn1034/CP0818/CPj1034 precursor.
CPN1034 OR CP0818 OR CPJ1034.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydophila pneumoniae).
NCBI TaxTn-Rqqqiales;
                                                        SEQUENCE FROM N.A.
                                                                                                                                        MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                               STRAIN=CWL029
                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                        CHLPN
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EMBL; U03858; AAA19825.1; --
EMBL; U29874; AAA99949.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QASSYTAPQP 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted (isoform 2).
ALTERNATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here) and 2/soluble; are produced by alternative splicing.
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60.0%;
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                               262 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                            J. B101. Chem. 260:8203-8213(1985).

11 FUNCTION: GLIADIN IS THE MAJOR SEED STORAGE PROTEIN IN WHEAT.

11 MISCELLANEOUS: THE ALPHA/BETA-GLIADINS CAN BE DIVIDED INTO 5.

12 HOMOLOGY CLASSES. SEQUENCE DIVERGENCE BETWEEN THE CLASSES IS DUE TO SINGLE BASE SUBSTITUTIONS AND TO DUPLICATIONS OR DELETIONS WITHIN OR NEAR DIRECT REPEATS. THERE ARE MORE THAN A 100 COPIES OF THE GENE FOR ALPHA/BETA-GLIADIN PER HAPLOID GENOME.
                                                                                                                                                                                                                                                                                                                                                                              "Evolution and heterogeneity of the alpha-/beta-type and gamma-type gliadin DNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINE=85234522; PubMed=2989281;

Okita T.W., Cheesbrough V., Reeves C.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P04724;
13-AUG-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum (Wheat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Alpha/beta-gliadin A-IV precursor (Prolamin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDA4_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 TAPQPQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shirai M., Hirakawa H., Kimoto M., Tauuuni M., Anton., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CRUA29 from USA."
Nucleic Acids Res. 28:2311-2314 (2000).
-I- SUBCELLULAR LOCATION: Outer membrane (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Outer membrane; Signal; Complete proteome. 1 	ext{ 17}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; CP0818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP002548; BAA99241.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 TAPQPQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.9%; Score 33; DB
100.0%; Pred. No. 61;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUTATIVE OUTER MEMBRANE PROTEIN CPN1034/CP0818/CPJ1034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 262; 61;
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OM protein - protein search, using sw model

January 13, 2003, 09:53:20; Search time 10.1538 Seconds (without alignments) 104.146 Million cell updates/sec

Title: Perfect score: Sequence: US-09-554-941-2 57 1 QASSYTAPQPQ 11

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR\_73:\*

1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

vative 0; Mismatches 0; Indels 0; ways	Matches 10; Conser  OY 1 QASSYTAPOP 10
; Length 728; 1; Table 0:	Query Match
F;65-89/Domain: Properties "Status experimental CMATY F;67-728/Product: galactose oxidase #status experimental F;107-116,604-607/Disulfide bonds: #status experimental F;107-116,604-607/Disulfide bonds: #status experimental F;317-361/Cross-link: cysteinyltyrosine (Cys-Tyr) #status experimental F;316,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,670/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,570/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,570/Binding site: copper (Tyr, Tyr, His, His) #status experimental copper F;361,584,585,570/Binding site: copper F;361,584,585,585,570/Binding site: copper F;361,584,585,585,57	F;65-8y/Domain: properties F;90-728/product: galactose oxidase F;90-728/product: galactose oxidase F;107-116,604-607/Disulfide bonds: F;107-116,604-607/Disulfide bonds: F;317-361/Cross-link: cysteinyltyros F;361,584,585,670/Binding site: copp F;419/Binding site: substrate (Arg)
C;Genetics: A;Gene: gaoA A;Gene: gaoA C;Superfamily: Cladobotryum dendroides galactose oxidase C;Superfamily: Cladobotryum dendroides galactose oxidoreductase C;Keywords: disulfide bond; metal binding; oxidoreductase C;Keywords: disulfide bequence status predicted <sig> F;1-64/Domain: signal sequence status predicted <pro></pro></sig>	C;Genetics: A;Gene: gaoA C;Superfamily: Cladoboti C;Keywords: disulfide bo C;Keywords: signal st F;1-64/Domain: signal st
R;ICO, N: FILTIFY, O. TO DATA BANK, September 1993 submitted to the Brookhaven Protein Data Bank, September 1993 A;Beference number: A51742; pDB:IGOH A;Beference number: A51742; pDB:IGOH A;Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 90-728	R; ITO, N.; FILLILES, Consulted to the Brookhal A; Reference number: A517 A; Contents: annotation;
phy,	submitted to the Brookhaven Protein submitted to the Brookhaven Protein A; Reference number: A51741; PDB:1GOG A; Reference number: X-ray crysta A; Contents: Languages F V · Knowles
ata Bank, lography, P.F.	submitted to the Brookhaven Protein submitted to the Brookhaven Protein S. 1, Reference number: A51740; Crysta A; Contents: annotation; X-ray Crysta D: Tro N: Phillips, S.E.V.; Knowles
Nature 350, 87-90, 1391 A;Title: Novel thioether bond revealed by a 1.7 angstrom crystal structure of garacom A;Title: Novel thioether bond revealed by a 1.7 angstrom crystal structure of garacom A;Title: Novel thioether bond revealed by a 1.7 angstrom crystal structure of garacom A;Tontents: annotation B: Trong Novel thiostopy (Noveles, P.F.)	Nature 350, 87-90, 1991 A; Title: Novel thioether bond reveale A; Reference number: A48244; MUID:9116 A; Referents: annotation A; Contents: annotation A; Contents: annotation A; Contents: annotation
GB:M86819 GB:M86819 ain whether Met-1 or Met-49 is the initiator ain whether met-1 or Met-49 is the initiator s sequence, including the amino end of the mature protein, s.E.V.; Stevens, C.; Ogel, Z.B.; McPherson, M.J.; Keen, S.E.V.; Stevens, C.; Ogel, Z.B.; McPherson, M.J.; Keen,	A; Residues: 1-728 < MCF > A; Residues: 1-728 < MCF > A; Cross-references: GB:M86819 A; Note: it is uncertain wheth A; Note: parts of this sequenc A; Note: parts of this sequenc A; Ito, N.; Phililips, S.E.V.;
RESULT 1  A38084 A38084 C;Becioes Oxidase (EC 1.1.3.9) precursor [validated] - fungus (Cladobotryum dendroide galactose oxidase (EC 1.1.3.9) precursor [validated] - fungus (Cladobotryum dendroide galactose Oxidase (EC 1.1.3.9) precursion 20-oct-2000 #text_change 20-Oct-2000 (;pate: 20-oct-2000 #sequence_revision 20-oct-2000 #text_change 20-Oct-2000 (;pate: 20-oct-2000 #sequence, C: Yadav, K.D.S.; Keen, J.N.; Knowles, P.F. C;Accession: A38084 A;Molecule type: DNA, A;Molecule type:	A38084 A38084 A38084 C;Species: Cladobotryum dendroides C;Species: Cladobotryum dendroides C;Date: 20-Oct-2000 #sequence_revi C;Accession: A38084 C;Accession: A38084 A;Title: Galactose oxidase of Dact A;Title: Galactose oxidase of Dact A;Reference number: A38084; MUID:9 A;Recession: A38084 A;Accession: A38084 A;Accession: A38084

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В
RESULT 4
                                                                                                                                                                                                                           A; Map position: 1
                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE001994; GB:AE000513; NID:g6459259; PIDN:AAF11071.1; PID:g645926
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: B75388
C;Accession: B75388
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.;
M.: Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
                                                                                                                                                                                                                                                   A; Gene: DR1504
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-224 <W
                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                       A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH dehydrogenase I, C subunit - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Introns: 83/3; 254/1; 355/2; 472/3; 548/1; 600/3; 650/1; 733/3; 843/2; 976/3; 1080/3; C:Superfamily: Caenorhabditis elegans hypothetical protein R10H10.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1416 <WI2>
A;Cross-references: EMBL:Z70686; PIDN:CAA94614.1; GSPDB:GN00022; CESP:R10H10.7
A;Experimental source: clone R10H10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 4
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, April 1996
A;Reference number: 219846
A;Accession: T24156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z70683; PIDN:CAA94594.1; GSPDB:GN00022; CESP:R10H10.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1-1416 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T20823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: Z19329
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                                                                                                                                                              Local Similarity
                                                                                                3 SSYTAPQPQ 11
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                                                                                                                                                                                                                                                                                                                               1-224 <WHI>
                                                                                                                                      Conservative
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                                                                                                                                                       68.4%;
77.8%;
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77.8%;
                                                                                                                                                     Score 39;
Pred. No. 7
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Pred. No. 34;
                                                                                                                             Mismatches
                                                                                                                                                                     DB 2;
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                                                                                                                                                              Length 224;
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A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                          protein R119.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: G87719
                                                                                                                 R;anonymous, The C. elegans Sequencing Consortium Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                    RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Accession: A13605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
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A;Experimental source: strain 16M
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A; Residues: 1-112 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potassium efflux system protein phaC [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
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A;Reference number: A73250; MUID:20036896; PMID:10567266
A;Accession: G75509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
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A; Residues: 1-90 <WHI>
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80.0%;
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Pred. No. 6.
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A; Accession: C87719
A; Accession: Preliminary
A; Status: Preliminary
A; Status: Lype: DNA
A; Molecule: 1-583 <570
A; Residues: 1-583
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C:Species: Streptococus pneumoniae
Penicils: Streptococus pneumoniae
C:Species: Strain 1951
A:Variety: Strain 1951
A:Variety: Strain 1951
C:Accession: John Jate (Library 1993)
R:Walted to: Wolecus (Library 1993)
R:Ribalted to: Wolecus (Library 1993)
R:Ribalton: Wolecus (Li
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A; Molecule 17139 <KEL>
A; Molecule 17139 <KEL>
A; Residues:
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                                                                                                                                                                                                                                                                            Query Match
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181 AYSYTAPGPE 190
                                                                                                           2 ASSYTAPOPO 11
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7; Conserve
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Score No. 47;
Pred. No. 1;
Mismatches
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                            score 36; DB 2;
pred. No. 47; 7; pred. No. 1; Mismatches
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A; Molecule type; DNA
A; Mosidues: 1-482 <KUR: AE008917; F
A; Residues: GB: AE008917; F
A; Cross : Teferences: GB: AFTAIN 16M
A; Experimental source: A; Cross imental source: A; Cross imental source: A; Experimental source: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Wolecule 1.513 CCHE A; Residues: 1.513 CCHE A; Resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Generics: Cyp24: GDB:134534; OMIM:600125

A; Gene: GDB:Cyp24: GDB:134534; OMIM:600125

A; Gene: Feteren Cos: 3-20013: 3 pas0 Cyp11B1; Cytochrome pas0 homology

A; Gene: Feteren Cos: 4-20013: 3 pas0 Cyp11B1; Cytochrome predicted cyrep-

A; Gene: Feteren Cos: 5-20013: 3 pas0 Cyp11B1; Cytochrome predicted predicted

A; Gross-psition: human cytochrome pas0 homology hydroxylase #status predicted

A; Map Permaily: chromoprotein: heme; (mitochond b) 24 hydroxylase

A; Map Permaily: chromoprotein: heme; heme logy 11gand) #status predicted

C; Keywordmain: t. 1, 25-dinhe pas0 homology 11gand) #status predicted

F; 36-513/Promain: Cytochrome pas0 (Cys) (axial ligand)

F; 36-483/Domain: cytochrome iron (Cys) (axial ligand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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1 6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
AB7372 1,4-beta-zylosidase [imported] - Caulobacter crescentus 10-May-2001
AB7372 1,4-beta-zylosidase [imported] - Caulobacter crescentus 20-Apr-2001 #text_change 10-May-2001
AB7371 1,4-beta-zylosidase [imported] - Capr-2001 #text_change 10-May-2001
AB7372 1,4-beta-zylosidase [imported] - Capr-2001 #sequence_revision 20-Apr-2001 #sequence_revision 20-Apr-2001
C;Accession: Callobacter current T.V.; paulsen, I.T.; beta-zylosidase [imported] - Callobacter 200 Apr-2001
C;Accession: Capr-2001
C;Accession: Capr-2001
C;Accession: Capr-2001
C;Accession: Capr-2001
R;Nierman, M.T.; beboy, R.T.; bodson, R.J.; burkin, A.S.; Gwinn, M.T.; beboy, R.T.; bodson, R.J.; burkin, A.S.; Capr-2001
R;Nierman, M.T.; beboy, R.T.; bodson, R.J.; burkin, A.S.; Capr-2001
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5; Conserv
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pred. No. 60; 2;
pred. No. 10; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 482;
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R'MCMUTTAY, A.
SUBMItted to the EMBL Data Library, November 1996
                                                                                                                                                                Typothetical protein KO8E3.1 - Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Accession: T23455 ** Sequence_revision 15-Oct-1999 ** text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                       A; Description:
C; Superfamily: it is essential for integration, replication-transposition, and excision
C; Reywords: DNA binding; DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-88
                                                                                                                                                                                                                                                                                                                                                                                                            TOSS, TEREFURES: EMBL: VOI464; NID:915807; PIDW:CAA24713.1; PID:915810
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Notice of the immunity region of bacteriophage Mu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross references GB:M11195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA Residues: 1-662 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Species: phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A novel DNA binding and nuclease activity in domain III of Mu transposase: evid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <sup>Asposase</sup> - phage Mu
Pecies: Phage Mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Cross: references: GB:AE005673; NID:913422273; PIDN:AAK22973.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 QADSFTAPIP 457
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70.08, Pred No.

 Indels

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hypothetical protein XF1117 (imported) - Xylella fastidiosa (c.)Species: Xylella fastidiosa (c.)Acces: 18 Aug -2000 fastidiosa (strain 9a5c) F. Acces: 18 Aug -2000 fastidiosa (strain 9a5c) fastidiosa (strain fastidiosa) fastidiosa (
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                                                                                                                                                                                                                                                                                                                                                                                                                        A. Status: Preliminary: Lranslated from GB/EMBL/DDBJ
A. Rosicule type: mRNA
A. Cross references: EMBL:U88539; NID:92754751; PID:92754752; PIDN:AAC40052.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Chlang, P.W.; Stubbs, L.; Zhang, L.; Kurnit, D.M.
A:Title: 47, 426-428, 1998
A:Title: Isolation of murine SPT5 homologue: Completion of the isolation and characte
                                                                                                                                                                                                                                                                                                                                                                                    883 OFSPYAAPSPO 893
                                                                                                                                                                                                                                                                                                                                                                                                       1 QASSYTAPOPO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tring structural protein homolog Suptshp - mouse /Accession: T42204 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7%,
Matches 6, Conservative
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                                                                                                                                                                                                157, 2000 Consortium of the Organization for Mucleotide Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status, preliminary, translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                         63.2%; Score 36; DB 2; Length 1082; o; Mismatches 4; Indels
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Vative 1; Pred. No. 86; DB 2; L
Mismatches 0;
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, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XFI117
Query Match 61.4%; Score 35; DB 2; Length 483; Best Local Similarity 63.6%; Pred. No. 92; Matches 7; Conservative 1; Mismatches 3; Indels
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В Qy 1 QASSYTAPQPQ 11 ||: ||| || 157 QATGATAPAPQ 167

0; Gaps

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Search completed: January 13, 2003, 09:57:09 Job time: 13.1538 secs

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